

GenCore version 5.1.4-p5_4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 11:25:23 ; Search time 7565 Seconds

(without alignments)
262.559 Million cell updates/sec

Title: US-10-070-464-1
Perfect score: 4700
Sequence: 1 MAAMETPQLGVEIFETADC.....HLHLHYQENLGSRIALAKVI 882

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Command line parameters: -DEV-xlp
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-DB-N.Geneseq_101002 -QFMT-fastap -SUFFIX-p2n.rng -MINMATCH-0.1 -DOORCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdl
-LIST-75 -DOCALLIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-30
-NODE-LOCAL -OUTFMT-pco -NOR-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US10070464.ecgn.1.1.396.ecunat_13052003_140014_29617 -NCPU-6 -ICPU-3
-NO_XLPRX -NO_WMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LOGLOG -DEV-TIMEOUT-120
-NARN-TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -Fgapop-6 -Fgapext-7
-YGAPOP-10 -YGAEXT-0.5 -DELOP-6 -DELEXT-7

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24: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4700	100.0	2671	24	ABK83322	CDNA encoding huma
2	4700	100.0	3106	24	ABK12892	Human protease PR
3	4700	100.0	3120	22	AAC85694	Nucleotide sequenc
4	4700	100.0	3120	24	AAD38856	Human dipeptidyl p
5	4700	100.0	3143	24	AAH99334	CDNA encoding 2195
6	4695	99.9	2643	24	AAH99335	Coding sequence of
7	4680	99.6	4829	24	ABK83327	CDNA encoding huma
8	4385.5	93.3	4685	24	ABK83332	CDNA encoding huma
9	4385	93.3	4676	24	ABK83331	CDNA encoding huma
10	4118	87.6	2842	24	ABK59774	Novel human coding
11	4092.5	87.1	4523	24	ABK83325	CDNA encoding huma
12	3970.5	84.5	2510	24	AAD23843	Human protease PR
13	3771	80.2	2668	24	ABK59775	Novel human coding
14	3661.5	77.9	4309	24	ABK83328	CDNA encoding huma
15	3364.5	71.6	2151	22	AAH15009	Human CDNA sequenc
16	2870	61.1	2617	24	ABK83323	CDNA encoding huma
17	2870	61.1	4219	24	ABK83335	CDNA encoding huma
18	2870	61.1	4302	24	ABK83333	CDNA encoding huma
19	2863	60.9	3024	24	AAD38854	Human dipeptidyl p
20	2835	60.3	2495	24	AAD38857	Human dipeptidyl p
21	2833	60.3	3287	24	AAD38855	Alternative versio
22	2820.5	60.0	4180	24	ABK83339	CDNA encoding huma
23	2820.5	60.0	4563	24	ABK83338	CDNA encoding huma
24	2763	58.8	2751	24	AAD38311	Murine dipeptidyl
25	2649	56.4	4076	24	ABK83337	CDNA encoding huma
26	2649	56.4	4159	24	ABK83336	CDNA encoding huma
27	2638	56.1	2801	22	AAI57896	Human polynucleoti
28	2599.5	55.3	4037	24	ABK83341	CDNA encoding huma
29	2599.5	55.3	4120	24	ABK83340	CDNA encoding huma
30	2476.5	52.7	3362	22	AAI57880	Human polynucleoti
31	2422	51.5	1669	22	AAC85966	Nucleotide sequenc
32	2226.5	47.4	2882	22	AAI59666	Human polynucleoti
33	1914.5	40.7	2461	21	AAC75835	Human ORF ORF190
34	1878.5	40.0	2952	24	ABK69090	DNA encoding huma
35	1874.5	39.9	3047	24	ABK69113	DNA encoding huma
36	1836.5	39.1	1083	22	AAC85697	Nucleotide sequenc
37	1645.5	35.0	1197	22	AAC85695	Nucleotide sequenc
38	1644.5	35.0	2027	21	AAC77137	Human ORF ORF2692
39	1599.5	34.0	3713	23	ABL10425	Drosophila melanog
40	1599.5	34.0	3783	23	ABL06641	Drosophila melanog
41	1400	29.8	2079	21	AAI37672	Human polynucleoti
42	1391	29.6	2411	24	ABK83334	CDNA encoding huma
43	1370.5	29.2	2034	22	AAI59682	Human polynucleoti
44	1360	28.9	6228	23	ABL10424	Drosophila melanog
45	1360	28.9	6228	23	ABL06640	Drosophila melanog
46	1351	28.7	1837	24	ABK69114	DNA encoding huma
47	1278	27.2	1356	24	ABK83326	CDNA encoding huma
48	1063	22.6	631	22	AAH07860	Human CDNA clone (
49	1026.5	21.8	832	24	ABK83330	CDNA encoding huma
50	929	19.8	873	22	AAE81719	Human protease and
51	927	19.7	925	24	ABL90148	Human polynucleoti
52	755.5	16.1	823	24	ABK30401	Human G-protein-co
53	736	15.7	1048	22	AAI41004	CDNA encoding nove
54	668	14.2	662	22	AAK93366	Human CDNA 5'-end
55	668	14.2	662	22	AAK93366	Human CDNA clone r
56	668	14.2	1748	22	AAK94819	Human full-length
57	665.5	14.2	561	22	AAI00876	Human reproductive
58	597.5	12.7	2313	20	AAK00013	Aspergillus oryzae
59	597.5	12.7	5496	20	AAH07327	Aspergillus oryzae
60	572	12.2	2199	21	AAH57338	Nucleotide sequenc
61	529	11.3	3407	24	ABK92227	Prostate cancer-as
62	526	11.2	2924	15	AAO63261	CDS26 CDNA clone.
63	525	11.2	2924	14	AAO46089	Sequence of human
64	524	11.1	4835	24	ABK63663	Rat sequence diffe
65	475.5	10.1	587	22	AAH12830	Human CDNA clone (
66	466.5	9.9	2505	23	ABL29869	Drosophila melanog
67	464	9.9	620	24	ABK83329	CDNA encoding huma

68	461	9.8	2388	24	ABA05888	Human aminopeptidase
69	461	9.8	2583	24	ABK83324	CDNA encoding huma
70	461	9.8	3238	24	ABA05887	CDNA encoding huma
71	461	9.8	4541	24	ABK83342	CDNA encoding huma
72	456.5	9.7	2967	23	ABL17649	Drosophila melanog
73	455	9.7	3224	24	AAS94862	Human DNA sequence
74	454	9.7	2814	24	ABL62162	Colon adenocarcino
75	454	9.7	2814	24	ABL63097	Breast cancer rela

ALIGNMENTS

RESULT 1
ABK83322
ID ABK83322 standard; cDNA; 2671 BP.

AC ABK83322;
XX
XX 12-AUG-2002 (first entry)
XX

DE CDNA encoding human DPPIV related serine protease DPP-1.

KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyslexia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.

XX Homo sapiens.
OS

XX WO200231134-A2.
PN

XX 18-APR-2002.
PD

XX 12-OCT-2001; 2001WO-US31874.
PF

XX 12-OCT-2000; 2000US-240117P.
PR

XX (FERR) FERRING BV.
XX

XX Qi S, Akinsanya KO, Riviere PJ, Junten J;
XX

DR WPI; 2002-444178/47.
DR

XX P-PSDB; ABG61591.
XX

PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT

PS Claim 1: Page 53-54; 113pp; English.
XX

CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyslexias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPPR proteins.
CC

SO Sequence 2671 BP; 805 A; 524 C; 594 G; 748 T; 0 other;

Alignment Scores: 0
Ptd. No.: 0

Length: 2671

Score:	4700.00	Matches:	882
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-070-464-1 (1-882) x ABK83322 (1-2671)

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QY	21	GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr	40
DB	68	GAGGAGAAATATTGAATCAGCAGATCCGCCCTAAATTGGAGCCTTTTATGTCGCGGTAT	127
QY	41	SerTrpSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet	60
DB	128	TCCTGGAGTCAGCTTAAAGCTGCTTGGCCGATACAGAAATATCATGCTCATGATG	187
QY	61	AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer	80
DB	188	GCTAAGCAGCACATGATTTTCATGTTGTGAAGAGATATCCAGATGACCTCATTC	247
QY	81	AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer	100
DB	248	GACGAGATCTATTACCTTCCCATGTGTGGAGAGACAGAAATATCAGCTTTTATTC	307
QY	101	GluIleProLysThrIleAsnArgAlaIleValLeuMetLeuSerTrpLysProLeuLeu	120
DB	308	GAAATTCCTCAAACTATCAATAGAGCAGCTTATGCTCTTGGAGAGCTCTTTTG	367
QY	121	AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg	140
DB	368	GATCTTTTCAGGCACACAGCTGACATGATGATATTCGAGAGAGACATTAAGA	427
QY	141	GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly	160
DB	428	GAAAGAAAGCATTGGAGACAGTCGGAAATGCTTTCATGATTAATCAGCAAGAGTGA	487
QY	161	ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyProGlnGly	180
DB	488	ACATTTCTGTTCAAGCGGTAGTGAATTAACGCTTAAGATGAGGAGCCACAGGA	547
QY	181	PheThrGlnGlnProLeuAspProAsnLeuValGluThrSerCysProAsnIleArgMet	200
DB	548	TTTACGCAACACCTTAAAGGCCCATCTAGTGAACATGTTGCCAACATACGATG	607
QY	201	AspProLysLeuGlyProAlaAspProAspTyrIleAlaPheIleHisSerAsnAspIle	220
DB	608	GATCCAAATTAATGCGCTGCTGATCCAGACTGGATGCTTTTATCATATCAACAGATATT	667
QY	221	TrpIleSerAsnIleValThrArgGluGluArgIleuArgIleuThrValHisAsnGluLeu	240
DB	668	TGATATATCAACATCGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA	727
QY	241	AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGln	260
DB	728	GCAACATGGAAGAAGATGCCAGATCAGCTGAGTGCCTTGTTCACAGAAAGAA	787
QY	261	PheAspArgTyrSerGlyTyrTrpTyrCysProLysAlaGluThrThrProSerGlyGly	280
DB	788	TTTGATATGATATCTGCTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	847
QY	281	LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal	300
DB	848	AAATATCTTAAGATCTATATGAGAAAGAAATGATGATGATGATGATGATGATGATG	907
QY	301	ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr	320
DB	908	ACATCCCTATGTTGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA	967
QY	321	AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle	340

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Db 1028 ATTAGATGTATGATVAGAGAACTAATTCAACTTTTGAGATTCCTATTGAGAGAGTTGAA 1087
QY 361 TYTLeaIaArgAlaGIuThrPThrProGIuGIuLySTyrAlaIlePserIleLeuLeuAsp 380
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QY 381 ArgSerGIuThrArgLeuGIuIleValIleuIleSerProGIuLeuPhelProValGIu 400
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QY 401 AspaAspValMetGIuArgGIuIleArgLeuIleGIuSerValProAspSerValThrProLeu 420
Db 1208 GATGATGTATGGAAGGAGAGACTCATTTGATGACTGCTGATTCCTGTGAGCCACTA 1267
QY 421 ILeIleTyrGIuGIuThrThrasPleIlePLeasNIleHisAspIlePhelHisValPhe 440
Db 1268 ATTATCTATGAGAAACACAGACATCTGATTAATATCATCATCATCTTTCATGTTTTT 1327
QY 441 ProGIuSerHisGIuGIuGIuIleGIuPhelIlePheAlaSerGIuCysLySThrGIuPhe 460
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QY 461 ArgHisLeuTyrLySThrSerIleLeuLySGIuSerLySTyrLySThrArgSerGIu 480
Db 1388 CGCATTTATACAAATTAATCTATTTTAAAGGAAGAAATVAAACGATCCACTGGT 1447
QY 481 GIuLeuProAlaProSerAspPheLySCysProIleLySGIuGIuIleAlaIleThrSer 500
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QY 501 GIuGIuThrGIuValIleuGIuArgHisGIuSerAsnIleGIuValAspGIuValArgArg 520
Db 1508 GGGAAATGGGAAGTCTTGGCGGCAATGATCAATATCCAACTGATGACAGACAGAAAG 1567
QY 521 LeuValTyrPheGIuGIuThrLySThrLySThrAspSerProLeuGIuHisIleLeuTyrValIleSer 540
Db 1568 CTGGTATATTGGAAGGACCAAGACTCCCTTTAGAGATCATCTGTACGTACAGTCACT 1627
QY 541 TyrValAsnProGIuGIuValIleThrArgLeuThrAspArgGIuTyrSerHisSerCysCys 560
Db 1628 TACGTAAATCCTGAGAGAGTGCACAAAGCTGACGCGGTACTACATTCCTGCTCAG 1687
QY 561 IleSerGIuHisCysAspPhePheIleSerLySTyrSerAsnGIuLysAsnProHisCys 580
Db 1688 ATCAGTCACAGCTGTCACTTTTATAGTAACTAATACAGAGAAATCCACACTGT 1747
QY 581 ValSerLeuTyrLySThrLeuSerSerProGIuAspAspProThrCysLySThrLySGIuPhe 600
Db 1748 GGTGCTCCCTTACAGCTATCAAGCTCTGTAGAGATGAGCCCAACTGGCAAAACAAAGAAATTT 1807
QY 601 TyrAlaIleThrIleLeuAspSerAlaGIuProLeuProAspTyrThrProProGIuIlePhe 620
Db 1808 TGGGCGACCATTTTGGATTCAGAGAGTCTCTCTGATATACCTGCTCAGAAATTTTC 1867
QY 621 SerPheGIuSerThrThrLySThrPheThrLeuTyrGIuMetLeuTyrLySThrProHisAspLeu 640
Db 1868 TCTTTTGAAGAACTACTGATTTTACATGTATGGGATCTCTACAGCCCTCATGTACTA 1927
QY 641 GIuProGIuLySTyrProThrValIleuPheIleTyrGIuGIuProGIuValGIuLeu 660
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QY 661 ValAsnAsnArgPheLySGIuValLySTyrPheArgLeuAsnThrLeuAlaSerLeuGIu 680
Db 1988 GTGAATATATGATTTTAAAGAGAGTCAAGTATTTCCGCTGAATACCTACAGCTCTAGAG 2047
QY 681 TyrValValValValIleAspAsnArgLySTyrCysHisArgGIuLeuLySThrPheGIuGIu 700
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Db 2048 TATGTGTTAGTATAGACAAACAGGGATCTCTGACCGAGGCTTAATTTGAAGGC 2107
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Db 2108 GCTTTTAAATATVAAATGGGTCAATAGAAATTTGACGATCAGGTGGAGAGACTCCAAATAT 2167
QY 721 LeuAlaSerArgTyrAspPheIleAspPheAspArgValGIuIleHisGIuTyrPserTyr 740
Db 2168 CTAGCTTCGATGATATTCATTGACTTAAGATCGTGTGGCATTCACAGGCTGTGCTCAT 2227
QY 741 GIuGIuTyrLeuSerLeuMetAlaLeuMetGIuArgSerAspIlePheArgValAlaIle 760
Db 2228 GGAGGATACCTCTCCCTGATGCGATTAAATGCAGAGCTCAGATATCTTCAGGCTTCTAAT 2287
QY 761 AlaGIuAlaProValThrLeuThrPheTyrAspThrGIuTyrThrGIuArgTyrMet 780
Db 2288 GCTGGGGCCCCAGTCACTGTGTGATCTTCAATGATACAGATACAGGAAACGTTATATTC 2347
QY 781 GIuHisProAspGIuAsnGIuGIuGIuTyrTyrLySThrArgGIuSerValAlaMetGIuAlaGIu 800
Db 2348 GGTACACCTGACAGATGACAGGGCTATTTACTTAGATCTGTGGCATGCACAGACAGAA 2407
QY 801 LysPheProSerGIuProAsnArgLeuLeuLeuLeuHisGIuPheLeuAspGIuAsnVal 820
Db 2408 AAGTTCCTCTGAACCAATCGTTTACTGCTTACATGTGTTTCCGTGATGAGAAATGTC 2467
QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGIuLySTyrProTyrAsp 840
Db 2468 CATTTTGCACATACCAATGATATTTATGAGTCTTGTAGTGAGGCTGAAACCATATATGAT 2527
QY 841 LeuGIuIleTyrProGIuGIuArgHisSerIleArgValProGIuSerGIuGIuHisTyr 860
Db 2528 TTACAGATCATCTCTCAGAGAGACACACAGCATTAAGGTTCTCTGAATCGGAGAACATTAT 2587
QY 861 GIuLeuHisLeuLeuHisTyrLeuGIuGIuAsnLeuGIuSerArgIleAlaIleLeuLyS 880
Db 2588 GAACCTCATCTTTTGCATACCTTCAAGAAACCTTGATCAGGTATTTGCTGCTTAATAA 2647
QY 881 ValIle 882
Db 2648 GTGATA 2653

RESULT 2
ABK12892
ID ABK12892 standard: cDNA: 3106 BP.
XX
AC ABK12892:
XX
DT 09-APR-2002 (first entry)
XX
DE Human protease PRS-9 cDNA sequence.
XX
KW Human: protease; PRS: gastrointestinal; Crohn's disease; cancer;
KW cardiovascular; atherosclerosis; autoimmune disorder; dermatitis;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW cell proliferative disorder; developmental disorder; epilepsy;
KW Duchenne muscular dystrophy; epithelial disorder; neurological disorder;
KW reproductive disorder; endometriosis; ss.
XX
OS Homo sapiens.
XX
FT key Location/Qualifiers
FT CDS 203..2851
FT FT /tag= a
FT FT /product= "Human protease PRS-9"
XX
XX WO200198468-A2.
XX
XX 27-DEC-2001.
XX
XX 13-JUN-2001: 2001WO-US19178.
XX
XX 16-JUN-2000: 2000US-212336P.
XX

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PR 22-JUN-2000: 2000US-213955P.
PR 29-JUN-2000: 2000US-215396P.
PR 07-JUL-2000: 2000US-216821P.
PR 14-JUL-2000: 2000US-218946P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Elliott VS, Gandhi AR, Lal P, Au-Young J, Tribouley CM;
PI Deleage AM, Baughn MR, Nguyen DB, Lee EA, Hafalia A, Khan FA;
PI Walla NK, Yao MG, Lu DM, Patterson C, Tang YT, Walsh RT;
PI Azimzai Y, Lu Y, Rankumar J, Xu Y, Reddy R, Das D, Kearney L;
PI Kallick DA;
DR WPI: 2002-090437/12.
DR P-PSDB: AAU74749.
XX
XX Twenty one human proteases (referred to as PRS-1 to PRS-21), useful
PT in the diagnosis, treatment and prevention of gastrointestinal (e.g.
PT gastritis), cardiovascular (e.g. atherosclerosis) and cell
PT proliferative (e.g. cancer) disorders -
PS
PS Claim 5; Page 166-167; 177pp; English.
XX
XX The present invention relates to twenty one new human proteases,
CC referred to as PRS-1 to PRS-21. The PRS polynucleotides and
CC polypeptides of the invention are useful in the diagnosis, treatment and
CC prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and
CC Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and
CC myocardial infarction, autoimmune/inflammatory e.g. acquired
CC immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell
CC proliferative e.g. cancer, developmental e.g. Duchenne and Becker
CC muscular dystrophy, epithelial e.g. dermatitis, neurological e.g.
CC epilepsy and Alzheimer's disease and reproductive e.g. infertility and
CC endometriosis disorders. Numerous other examples of each disorder are
CC given in the specification. The present nucleic acid sequence encodes
CC the human protease PRS-9 protein of the invention.
XX
XX Sequence 3106 BP: 928 A; 633 C; 704 G; 841 T; 0 other:
SQ
Alignment Scores:
Pred. No.: 0 Length: 3106
Score: 4700.00 Matches: 882
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-070-464-1 (1-882) x ABK12892 (1-3106)
QY 1 MetAlaAlaMetGluThrGluGluGluValGluIlePheGluThrAlaAspCys 20
DB 203 ATGGCAGCAGCAATGGAACAGAACACCTGGCTTGAGATATTTGAAACGCGACGT 262
QY 21 GluIuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 40
DB 263 GAGGAGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 322
QY 41 SerTrpSerGluLeuLysLysLeuAlaAspThrAlaGlyLysGlyLysMetMet 60
DB 323 TCCTGGAGTCACTTAATAAGCTCTTGGCATACCAAGAAATATCATGGTATATG 382
QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
DB 383 GCTAAGCACCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 442
QY 81 AspArgIleLeuThrLeuAlaMetSerGlyLysAsnArgLysAsnThrLeuPheTyrSer 100
DB 443 GACGAAATCTAATACCTTGCATGCTGGTGAAGACAGAGAAATATCATGGTATAT 502
QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
DB 503 GAATTCGCCAAACTATCATATAGACAGCACTTAAATGCTCTTGGAGCCCTTTTG 562

QY 121 AsPheGluAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
DB 563 GATCTTTTCAGGCACACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGluGlySerGly 160
DB 623 GAAAGAAACGATTTGAGACAGTGGAAATTCCTTACGATTTACCAAGAGAGTGA 682
QY 161 ThrPheLeuPheGluAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGluGly 180
DB 683 ACATTTCTGTTTCAAGCCGAGTGAATTTATACGTAAAGATGAGGCGCCCAAGGA 742
QY 181 PheThrGluGluProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
DB 743 TTTACGCAACACCTTTAAGGCCCAATCTAGTGAACATGATGTTCCCAACATCGCATG 802
QY 201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAspIle 220
DB 803 GATCCAAATTTATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 862
QY 221 TrpIleSerAsnIleValThrArgGluGluArgGlyLeuThrTyrValHisAsnGluLeu 240
DB 863 TGGATATCTAATCATCTGTAACAGAGAAAGAGAGACTCTTATGTCCACATGACCTA 922
QY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGluGlu 260
DB 923 GCCAACTGGAAGAGATGCGCATGACGTGACGTGACGTGACGTGACGTGACGTGAC 982
QY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGly 280
DB 983 TTTATATGATTTTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1042
QY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
DB 1043 AAATTTCTTAATCTATATGAGAAAGAAATGATCAATCTGAGTGGAAATTTATTCAGT 1102
QY 301 ThrSerProMetLeuGluThrArgAlaAspSerPheArgTyrProLysThrGlyThr 320
DB 1103 ACATCCCTATGTTGGAACAGAGAGGAGATTCATTCCTGTTAAACAGGTACA 1162
QY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluArgIle 340
DB 1163 GCAATCTTAAAGCACCTTTAAAGATGTCAAAATATGATGATGATGATGATGATGAT 1222
QY 341 IleAspValIleAspLysGluLeuIleGluProPheGluIleLeuPheGluGlyValGlu 360
DB 1223 ATGATGTGATAGATTAAGAACTAATTCACCTTTTGAGTTCATTTGGAAGGTTGAA 1282
QY 361 TyrIleAlaArgAlaGlyTyrPheProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
DB 1283 TATATTCACAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342
QY 381 ArgSerGluThrArgLeuGluIleValLeuIleSerProGluLeuPheIleProValGlu 400
DB 1343 CGCTCCAGACTGCTACAGATATGATGATGATGATGATGATGATGATGATGATGAT 1402
QY 401 AspAspValMetGluArgGluArgLeuIleGluSerValProAspSerValThrProLeu 420
DB 1403 GATGATGTTATGGAAGCAGAGAGCTCATTTGAGTCACTGCTGATGATGATGATGAT 1462
QY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
DB 1463 ATTATCTATGAGAAACAGACATCTGATTAATTCATGACATCTTCAATGTTT 1522
QY 441 ProGluSerHisGluGluGluIleGluPheIlePheAlaSerGlyCysLysThrGlyPhe 460
DB 1523 CCCAAAGTCAAGAGAGGAAATTTGATTTATTTTCTCTGATGATGATGATGATGAT 1582
QY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
DB 1583 CGTATTTATACAAATTTATCATCTATTTTAAAGAAAGCAATTAACATCAGAGGT 1642
QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500


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Db 1643 GGGCTGCTCCTCCAGTCAATGATTCATGCTCCATCAAGAGAGAGATAGCAATACCAGT 1702
Qy 501 G1G1u1rpfLuva1LeuG1yArGh1Sg1SerSnp1Leg1nva1Asp1G1u1Va1Arg 520
Db 1703 GGGAAATGGGAAGTCTTGGCCGGCATGATCTAATATCCAAAGTTGATGAAGTCAGAGG 1762
Qy 521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisLysLeuTyrValSer 540
Db 1763 CTGGTATATTTTGAAGCACCAGCAAGACTCCCTTTAGAGCATCCCTGACGTAGTGTAGT 1822
Qy 541 TyrValAsnProGlyGluVal1ThrArgLeuThrAspArgGlyTyrSerHisSerCys 560
Db 1823 TACGTAATCTGGAGAGAGTACAGACAGCTGACTGACCTGGCTACTGACATCTTGGCTGC 1882
Qy 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
Db 1883 ATCAGTCAGACGTGTGCTCTTATATAGTAATAGTAACCAAGAAATCCACACTGT 1942
Qy 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
Db 1943 GTGGCCCTTTACAGCATATCAAGCTCCAGAGATGACCCCACTTCCAAACAGAGATTTT 2002
Qy 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
Db 2003 TGGGCCACCAATTTGGATTCAGCAGGTCTCTCTGACTATACTCTCCAGAAATTTTC 2062
Qy 621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
Db 2063 TCTTTTAAAGTACTACTGATGATTTTACATTTATGGAGATGCTTCAAGACCTCAGATCTA 2122
Qy 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
Db 2123 CAGCCTGGAAAGAAATCTCTACTGCTGTTCATATATGGTGTCTCCAGGTCACTTG 2182
Qy 661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
Db 2183 GTGAATATGGGTTTAAAGAGTCATAGTATTTCCGCTTGATACCTCCTCTAGGT 2242
Qy 681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
Db 2243 TATGTGTTTGTAGTATGATACACAGAGGAGTCTGTCCAGGAGCTTAAATTTGAAGGC 2302
Qy 701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGlyGlyLeuGlnTyr 720
Db 2303 GCCTTAAATATAAATGGGCAATAGAAATGACATCAGTCAGTGAAGGACTCCTCAATAT 2362
Qy 721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTyrPheTyr 740
Db 2363 CTACCTTCTGATATGATTTTCAATGATGATGCTGGGCATCCACGCTGCTCAT 2422
Qy 741 G1y1y1rLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
Db 2423 GGAAGATACCTCCCTCGATGCGCATTAATGCAGAGTCAATATCTTCAAGGTTGCTATT 2482
Qy 761 AlaGlyValProVal1ThrLeuTyrPheTyrAspThrGlyTyrThrGluArgTyrMet 780
Db 2483 GCTGGGCCCCAGTCACTGTGTGATCTTCTATATACAGATACAGGAACGTTATATG 2542
Qy 781 G1yHisProAspGlnAsnGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
Db 2543 GGTACACCTCAACGAATGAAGAGGCTATATTACTTACGATCTGGCCATGCACAGCAAGAA 2602
Qy 801 LysPheProSerGluProAsnArgLeuLeuLeuHisGlyPheLeuAsnGluAsnVal 820
Db 2603 AAGTCCCTCTGACCAAAATCGTTTACTGTCTTACATAGGTTTCCGAGAGAAATGTC 2662
Qy 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
Db 2663 CATTTTGCACATACCACTATATATTCTAGTATTTTACTGAGGCTGGAAGCCCATATGAT 2722
Qy 841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGlnHisTyr 860

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Db 2723 TTACAGATCTATCTCAGAGAGACACAGCATAGACTTCTCGAATCGGAGAACATTAT 2782
Qy 861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuLysSerArgIleAlaLeuLys 880
Db 2783 GAACGCACTCTTTTGGCACTTCAAGAAACCTTGATCAGTATTTGCTCTAATA 2842
Qy 881 ValIle 882
Db 2843 GTGATA 2848

RESULT 3
AAC85694
ID AAC85694 standard; cDNA; 3120 BP.
XX
AC AAC85694:
XX
XX 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of human DPP8.
XX
KW Human; dipeptidyl aminopeptidase; DPP8; prolyl oligopeptidase;
KW dipeptidyl peptidase; DPPIV; T cell; cleavage; diarrhoea;
KW growth hormone deficiency; glucose level; mucosal regeneration;
KW non-insulin dependent diabetes mellitus; glucose intolerance;
KW immunosuppression; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..2862
FT FT /*lag= a
FT FT /product= "Human DPP8"
XX
XX MO200119866-A1.
XX
XX 22-MAR-2001.
XX
XX 11-SEP-2000; 2000MO-AU01085.
XX
XX 10-SEP-1999; 99AU-0002762.
XX 18-FEB-2000; 2000AU-0005709.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Abbott CA, Gorell MD;
XX
XX WPI; 2001-281520/29.
XX
XX P-PSDB: AAB47187.
XX
XX
XX New human dipeptidyl aminopeptidase (DPP8) useful for cleaving
XX substrates, identifying inhibitors of DPP8 catalytic activity which
XX have therapeutic uses, and for detecting activated T cells
XX
XX Claim 16; Fig 2; 78pp; English.
XX
XX This sequence encodes human dipeptidyl aminopeptidase (DPP8). DPP8
XX has substrate specificity for H-Ala-Pro-pNA, H-Gly-Pro-pNA and
XX H-Arg-Pro-pNA. Therefore, it is a prolyl oligopeptidase and a
XX dipeptidyl peptidase, because it is capable of hydrolysing the
XX peptide bond C-terminal to Pro in each of these compounds. DPP8
XX is homologous with human DPPIV. DPP8 is useful for cleaving a
XX substrate, and for detecting an activated T cell which involves
XX measuring the level of DPP8 gene expression in a T cell. The level
XX of DPP8 expression is detected by detecting the amount of DPP8 RNA
XX in the cell. It is also useful for identifying a molecule capable
XX of inhibiting the cleavage of the substrate by DPP8. Molecules
XX identified as inhibiting DPP8 catalytic activity may be useful for
XX treating diarrhoea, growth hormone deficiency, lowering glucose levels
XX in non-insulin dependent diabetes mellitus and other disorders
XX involving glucose intolerance, enhancing mucosal regeneration and
XX as immunosuppressants.
XX
XX Sequence 3120 BP; 936 A; 637 C; 706 G; 841 T; 0 other;

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Alignment Scores:

Pred. No.:	0	Length:	3120
Score:	4700.00	Matches:	882
Percent Similarity:	100.008	Conservative:	0
Best Local Similarity:	100.008	Mismatches:	0
Query Match:	100.008	Indels:	0
DB:	22	Gaps:	0

US-10-070-464-1 (1-882) x AAC85694 (1-3120).

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OY 1 MetAlaAlaMetGluThrGluGluLeuGluGluIlePheGluThrAlaAspCys 20
    |||
Db 214 ATGCAGAGCAATGGAACAGAACAGACGCTGGCTTGGATATTGAAACGCGACATG 273
OY 21 GluGluAsnIleGluSerGluAspArgProLysLeuGluProPheTyrValGluArgTyr 40
    |||
Db 274 GAGGAGATATTGATATACAGAGATGCGCTAAATTGGAGCTTTTATGTGGAGCGGTAT 333
OY 41 SerTrpSerGluLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
    |||
Db 334 TCCTGGAGTCACTTAAACAGCTGCTTCCGATACAGAAATATCATGGCTACATGATG 393
OY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
    |||
Db 394 GCTAAGGACACCATGATTCATGTTGTGTAAGAGGAATGATCCAGATGGACCTCATTTCA 453
OY 81 AsparGlyIleTyrTyrLeuAlaMetSerGlyLysAsnArgLysAsnThrLeuPheTyrSer 100
    |||
Db 454 GACGAGATCTTATACCTTCCATGCTGGTGAGAACAGAAATACCTCTTTTATTTCT 513
OY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
    |||
Db 514 GAAATTCCTCAAAACATCAATAGAGAGACAGCACTTAATGCTCTCTGGAAACCTCTTTTG 573
OY 121 AspleuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
    |||
Db 574 GATCTTTTTCAGGACACGCTGATGAAATGATTCCTCAGAAAGAACTATTAGA 633
OY 141 GluArgLysArgGlyLeuThrValGlyIleAlaSerTyrAspTyrHisGlySerGly 160
    |||
Db 634 GAAAGAAACCATTTGGACAGCTGGAATTCCTTTCATTCACCAAGAGAACTGGA 693
OY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
    |||
Db 694 ACATTTCTGTTTCAAGCGGAGTGAATTTATCAGCTAAAGATGAGGGCCCAACAGA 753
OY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
    |||
Db 754 TTTAGGCAACACCTTTAGGCCCAATCTAGTGAACACTAGTTGCTCCCAACATACGGATG 813
OY 201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
    |||
Db 814 GATCAAAATATATGCCCCGCGATCCAGACAGCTGATTCCTTTATATACAGCAAGCATATT 873
OY 221 TrpIleSerAsnIleValThrArgGluGluArgLeuThrTyrValHisAsnGluLeu 240
    |||
Db 874 TGGTATCTATACATCTAGTACAGAGAGAAAGAGAGACTCATTAATGTCCACAAATGAGCTA 933
OY 241 AlaAsnMetGluLysAspAlaArgSerAlaGlyValAlaThrPheValLeuGluGlu 260
    |||
Db 934 GCCAACATGGAAGAGATGCGATCAGATCAGCTGAGTCTGCTACCTTTGTTCTCCAGAAAGAA 993
OY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
    |||
Db 994 TTTGATATGATTTCTGCTGATTTGCTGCTGCTCAAAAGCTGAAACACATCCCAAGTGGT 1053
OY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspLysSerGluValGluIleIleHisVal 300
    |||
Db 1054 AAAATTTCTTAAATCTATATGAGAGAAATATGATCAATCTGAGTGGAAATTTATTCACTTT 1113
OY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
    |||
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Db 1114 ACATCCCTATGTGGAAACAGAGGACAGATTCATCCCTTATCCTAACAGAGTACA 1173
OY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
    |||
Db 1174 GCAATCTTAAGTACACTTATAGATGTCAGAAATATGATGATGCTGGAAGAGGATTC 1233
OY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
    |||
Db 1234 ATAGATGTCATAGATTAAGAGACTAATTCACCTTTTGAGATTCTATTGGAAGAGCTTGA 1293
OY 361 TyrIleAlaArgAlaGlyTyrThrProGluLysTyrAlaTrpSerIleLeuLeuAsp 380
    |||
Db 1294 TATATGGCAGAGCTGGATGACCTCTGAGGAGAAATATGCTGCTCATCTCTAGAT 1353
OY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
    |||
Db 1354 CGCTCCAGACTCCGCTTACATATGTTGATGCTCAGCTGATTTATTTCCAGTGA 1413
OY 401 AsparValMetGluArgGluArgLeuIleGluSerValProAspSerValThrProLeu 420
    |||
Db 1414 GATGATGTTATGGAAGGACAGACTCATTTGACAGTGCCTGATTCGTGACGCCACTA 1473
OY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
    |||
Db 1474 ATTAATCTATGAAGAAACACAGACATCTGATTAATATCCATGACATCTTTCATGTTTTT 1533
OY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
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Db 1534 CCCAAAGCTCAGAGAGAAATGATTTATTTTGGCTCTGATGCAAAACAGGTTTC 1593
OY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
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Db 1594 CGTCATTTATACAAATATACATCTATTTTAAGAGAAAGCAATATTAACGATCCAGTGGT 1653
OY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
    |||
Db 1554 GGGCTGCTGCTCCAGAGATTTCAAGTCTCTTCAAGAGGAGATTAACATTAACAGT 1713
OY 501 GlyIleTrpGluValIleGluArgHisGlySerAsnIleGlnValAspGluValArg 520
    |||
Db 1714 GGTGATGAGGAAGTCTTGGCGGCGATGATCTAATCCAGTGAATGAAAGTACGAAG 1773
OY 521 LeuValTyrPheGluGlyThrLysAspSerProLeuGlnHisLysLeuTyrValIleSer 540
    |||
Db 1774 CTGCTATATTTTGAAGCAGCAACCAAGCTCCCTTTAAGATCAGCTGATGATGAT 1833
OY 541 TyrValAsnProGluGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
    |||
Db 1834 TACGTAAATCTCTGAGAGAGTGACAGGCTGACTACCGTGGCTACTCACATTTCTTGGCTGC 1893
OY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
    |||
Db 1894 ATCAGTCAAGCTGCTGACTTCTTATAGTATAGTATAGTAAACGAAATCCACTGCT 1953
OY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
    |||
Db 1954 GTGTCCCTTTCAAGCTATACAGTCCGAGAGATGACCAACTGTCACAAACAAAGAAATTT 2013
OY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuArgProAspTyrThrProProGluIlePhe 620
    |||
Db 2014 TGGGCACACATTTTGGATGACAGAGTCTCTCTCTCATATACCTCTCCAGAAATTTTC 2073
OY 621 SerPheGluSerThrThrGluPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
    |||
Db 2074 TCTTTTGAAGTACTACTGATTTACATTTGATGGATGCTCTACAAAGCCATGATCTA 2133
OY 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
    |||
Db 2134 CAGCCTGGAAGAAATATCTACTGCTGCTGTATATATGATGCTGCTCAGGTCAGATTG 2193
OY 661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
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Db 2194 GTGAATATCGCTTTAAAGAGTCAAGTATTTCCGCTTGAATACCCATGAGCTCTAGGT 2253
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QY 681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly
    |||
Db 2254 TATGTGCTTGTAGTATGACACACAGGGGATCCGTGCACCGAGGGCTTAATTTGAAGGC 2313
QY 701 AlapheLysTyrLysMetGlyGlnIleGluIleAspAsnValGluGlyLeuGlnTyr 720
    |||
Db 2314 GCCTTTAATATATAAAGGCGCAATAGAAATGACATGACATGAGGAGGACTCCAAATAT 2373
QY 721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTyrSerTyr 740
    |||
Db 2374 CTACCTTCTCGATATGATTTTCATTGACTTATGATGCTGTGGCATCCACGGCTGCTCTAT 2433
QY 741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
    |||
Db 2434 GGAGGATACCTCTCCCTGATGGCATTAATGACAGAGTCAGATATCTTCAGAGTGTCTATTT 2493
QY 761 AlaglyAlaProValIlePheLeuTyrPheTyrAspPheArgGlyTyrGlnArgTyrMet 780
    |||
Db 2494 GCTGGGCCCCAGTCACTGTGTGATCTTCTATGATACAGATACAGGAAACGTTATATG 2553
QY 781 GlyHisProAspGlnAsnGlnGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
    |||
Db 2554 GGTACCCCTGACCGATGAACAGGCTATTACTTAGGATCTGTGGCATGCAACGAGAA 2613
QY 801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
    |||
Db 2614 AAGTTCCTCTGMAACCAATCGTTTACTGCTTACATGATGTTCTCGATGAGAAATGTC 2673
QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
    |||
Db 2674 CATTTTCACATACACATATATTAATGATTTTACTGAGGCTGGAAAGCCCAATATGAT 2733
QY 841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGlnSerGlyGlnHisTyr 860
    |||
Db 2734 TTACAGATCATCTCTGAGAGAGACACATAGACTTCTGATAGCGGAGAACATTAT 2793
QY 861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaIleLeuLys 880
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Db 2794 GAATGTCATCTTTTGCACCTCACTCACTTCAGAAACCTTGATCAGCATGATGCTCTAATA 2853
QY 881 ValIle 882
    |||
Db 2854 GTGATTA 2859

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RESULT 4
AAD38956
ID AAD38956 standard: cDNA: 3120 BP.
AC AAD38956;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human dipeptidyl peptidase 8 (DPP8) cDNA.
KW Human: dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW antiviral; enzyme; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..2862
FT /*tag= a
FT /product= "Human DPP8 protein"
XX
PN M0200234900-A1.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001: 2001MO-AU01388.
XX

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PR 27-OCT-2000: 2000AU-0001078.
PA
XX (UNSY ) UNIV SYDNEY.
XX
PI Abbott CA, Gorrell MD:
XX
DR WPI: 2002-454646/48.
DR P-PSDB: AAE24170.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Example: Fig 1; 91pp: English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polypeptides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immuno deficiency virus) infection. The present
CC sequence is human DPP8 cDNA.
XX
SQ Sequence 3120 BP: 936 A; 637 C; 706 G; 841 T; 0 other:

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Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0	3120	882	0	0	0
Percent Similarity:	4700.00					
Best Local Similarity:	100.00%					
Query Match:	100.00%					
DB:	24					

US-10-070-464-1 (1-882) x AAD38956 (1-3120)

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QY 1 MetAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
    |||
Db 214 ATGCACACAGCAAGGAAACAGAACACCTGGCTTGAGATTTGAAACGCGACACTGT 273
QY 21 GluGlnAsnIleGlnSerGlnAspArgProLysLeuGlnProPheTyrValGluArgTyr 40
    |||
Db 274 GAGGAGAAATATTGAATACACAGATCGGCTTAATTTGAGCTTTTATGTGACGGGAT 333
QY 41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
    |||
Db 334 TCCGTGAGTCAAGCTTAAAGAGCTTGGCCGATACCGAAATATCATGCGTACATGATG 393
QY 61 AlaLysAlaProHisAspPheMetCpheValLysArgAsnAspProAspGlyProHisSer 80
    |||
Db 394 GCTAAGCACACACATGATTCATGTTTGTGAAGAGAAATGATCCAGATGACACTCATTTCA 453
QY 81 AspArgIleTyrTyrLeuAlaIleMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
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Db 454 GACAGAAATCTATTAACCTTCCCATGTGTGTGAGAACAGAAATACAGCTTTTATTTCT 513
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Qy 881 Valille 882
Dh 2854 GTGATA 2859
RESULT 5
AAH9934
ID AAH9934 standard; cDNA: 3143 BP.
xx

AAH99934;
 12-APR-2002 (first entry)
 cDNA encoding 21953 human prollyl oligopeptidase.
 21953 prollyl oligopeptidase; human; proline; endopeptidase;
 cancer; cardiovascular disease; autoimmune disease; atopic allergy;
 neuronal disorder; vascular disorder; prostate disorder; cytostatic;
 antidiabetic; antihypertensive; antidiabetic; antiinflammatory;
 diabetes mellitus; arthritis; multiple sclerosis; asthma;
 Grave's disease; neuronal disorder; demyelinating disease; ss.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 229..2877
 /tag="a" "21953 prollyl oligopeptidase"
 /product="This region is specifically claimed in
 claim 2"
 WO200179473-A2.
 25-OCT-2001.
 11-APR-2001: 2001WO-US40483.
 18-APR-2000: 2000US-197508P.
 (MILL-) MILLENNIUM PHARM INC.
 Meyers RA, Williamson M;
 MPI: 2002-034353/04.
 P-PDB: AAC78415.
 New polypeptides 21953, member of human prollyl oligopeptidase family,
 useful as diagnostic targets and therapeutic agents for controlling
 cancer, lymphoma and leukemia
 Claim 7: Page 100-102: 121pp; English.
 This invention relates to an isolated 21953 human prollyl
 oligopeptidase, which is cytosolic, antidiabetic, antihypertensive,
 neuroprotective, antihypertensive, dermatological, antipsoriatic,
 antidiabetic, ophthalmological, antiinflammatory, nootropic,
 antiparkinsonian, anticonvulsant, gynaecological, vasorelaxant,
 antidiabetic, antidiabetic, antidiabetic, anorectic and
 metabolic in its action. Uses include gene therapy, expression or
 activity of 21953 protein modulator, it is useful for identifying a
 compound which binds to it and can be used in preventing, treating
 or detecting a cellular proliferative or differentiative disorder.
 The 21953 molecules can act as novel diagnostic targets and therapeutic
 agents for controlling disorders associated with the aberrant activity
 or degradation of peptide hormones e.g., disorders associated with cell
 differentiation and proliferation such as cancer, immune function,
 reproductive, neurological and cardiovascular function. The 21953
 molecules are thus useful for treating and preventing cellular
 proliferative and differentiative disorders, haematopoietic neoplastic
 disorders, immune disorders such as autoimmune diseases, diabetes
 mellitus, arthritis, multiple sclerosis, asthma, Grave's disease,
 neuronal disorders, demyelinating diseases, vascular disorders and
 metabolism or pain disorders. This sequence represents the cDNA
 encoding sequence of 21953 human prollyl oligopeptidase.
 SO Sequence 3143 BP; 943 A; 644 C; 712 G; 844 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 3143
 Score: 4700.00 Matches: 882
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
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DB 289 GAGGAGAAATATTGAATCAGACGATGCGCTTAAATGTGAGGCTTTTATGTGTGAGCGGTAT 348			
QY 41 SerTrpSerGlnLeuLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60			
DB 349 TCCTGGACGTACGCTTAAAGACGCTTCCGATACAGAAATATCATGCTCATGATG 408			
QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80			
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QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320			
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 RESULT 6
 AAH99935 standard; cDNA; 2643 BP.
 ID AAH99935 standard; cDNA; 2643 BP.
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 DT 12-APR-2002 (first entry)
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 KW 21953 prolyl oligopeptidase; antibody; proline; endopeptidase;
 cancer; cardiovascular disease; autoimmune disease; atopic allergy;
 neuronal disorder; vascular disorder; prostate disorder; cytostatic;
 antidiabetic; antiarthritic; antiasthmatic; antiinflammatory;
 diabetes mellitus; arthritis; multiple sclerosis; asthma;
 Grave's disease; neuronal disorder; demyelinating disease; ss.
 KW
 OS Homo sapiens.
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 PN WO200179473-A2.
 XX
 PD 25-OCT-2001.
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 PF 11-APR-2001; 2001WO-US040483.
 XX
 PR 18-APR-2000; 2000US-197508P.
 PA (MILL-) MILLENNIUM PHARM INC.
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 PI Meyers RA, Williamson M;
 DR WPI: 2002-034353/04.
 DR P-PSDB; AAG78415.
 XX


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Db 2461 TTTGCAATACAGACTATATTAATTAAGTATTTTATGAGGGCTGGAAAGCCATATGATTTA 2520
QY 842 GlnIleTyrProGluGluArgHisSerIleArgValProGluSerGlyGluHisTyrGlu 861
Db 2521 CAGATCTATCTCTGAGAGACACAGACATAAAGTCTCTGAAATCGGAGAAACATTATGAA 2580
QY 862 LeuHisLeuLeuHisTyrLeuGluGlnLysLeuGluSerArgIleAlaIleLeuLysVal 881
Db 2581 CTGCATCTTTTGGACTACTCTTCAAGAAACCTTGATCAGTATTTGCTGTCTTAAAGTG 2640

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QY 882 Ile 882
Db 2641 ATA 2643

RESULT 7
ID ABR83327 standard; cDNA: 4829 BP.
XX
AC ABR83327;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPP-1 splice variant #3.
XX
KW Human: serine protease; dipeptidyl peptidase IV-related protein; DPP;
KW DPP-IV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR ) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junten J;
XX
DR WPI: 2002-444178/47.
XX
PT P-PSDB; ABR61596.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT
XX
PS Disclosure: Page 65-66; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related
CC proteins (DPP-IV). The dipeptidyl peptidase IV-related proteins (DPP-
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABR83327-ABR83343 encode human DPP-IV proteins.
XX
SQ Sequence 4829 BP; 1466 A; 886 C; 1017 G; 1460 T; 0 other;

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Alignment Scores:

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Pred. No.: 0 Length: 4829
Score: 4680.00 Matches: 882
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.57% Indels: 2
DB: 24 Gaps: 0

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US-10-070-464-1 (1-882) x ABR83327 (1-4829)

QY 1 MetAlaAlaIaIaMetGluThrGluGluGluValGluIlePheGluThrAlaAspCys 20
 Db 214 ATGCAGACAGCAATGGAACAGAACAGCTGGTGGATATTGGAACCTGGGAGCTGT 273
 QY 21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyValGluArgTyr 40
 Db 274 GAGGAAATATTAATCAACAGATCGCCCTAAATTTGAGCCTTTTATGCTTGGCGGTAT 333
 QY 41 SerTrpSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
 Db 334 TCCTGGAGTCAGCTTAAAAAGCTGCTTCCGATACCGAAATATATCATGGCTCATGATG 393
 QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
 Db 394 GCTAAGGACACACATGATTTTCATGTTTGTGACAGAGAAATGATCCAGATGGACCTCATCA 453
 QY 81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgLysAsnThrLeuPheTyrSer 100
 Db 454 GACAGAAATCTATTACCTTGGCATGTCTGTGAGAACAGAAATAATACACTGTTTATTTCT 513
 QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
 Db 514 GAAATTCGCCAAACTATCATATAGACGACAGCTTTAATGCTTCTTGGAAAGCCTCTTTTG 573
 QY 121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetLysSerArgGluGluLeuLeuArg 140
 Db 574 GATCTTTTCAGGACACACTGACGACTATGGAATGATATTCGAGAGAAAGAACTATTAGA 633
 QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnIleSerGly 160
 Db 634 GAAAGAAACGCAATTTGGAAGAGTCGGAAATTTGCTTACATTAATCCCAAGAAAGTGA 693
 QY 161 ThrPheLeuPheGlnIleArgSerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
 Db 694 ACATTTCTGTTTAACCCGCTAGTGCATTTATCACCTTAAGATGGAGGCGCACAGGA 753
 QY 181 PheThrGlnGluProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
 Db 754 TTTTACGCAACACCTTTAAGGCCCAATCTAGTGAACCTAGTTGCCAACATACGAGATG 813
 QY 201 AspProLysLeuCysProAlaAspProAspTrpIleAlaIleHisSerAsnAspIle 220
 Db 814 GATCCAAATTAATGCTGCTGTATCCAGACTGATGCTTTTATACCTACCAACGAAATTT 873
 QY 221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
 Db 874 TGGATATCTTAACATCGTAACACAGAAAGAAAGAGACTCACTTATGTGCACATGACTTA 933
 QY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
 Db 934 GCCAATGAGAAAGATGCGCAGATCAGCGAGTCCGCTTGTTCACAAAGAA 993
 QY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaLeuThrThrProSerGlyGly 280
 Db 994 TTTGATATGATATTTCTGTATGTGTGTGTCAAAAGCTGAAACACTCCAGGCGGT 1053
 QY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
 Db 1054 AAATATCTTAAGATTTCTATATGAAAGAAATGATGATCTAGGTGCAATTTATTCATGTT 1113
 QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysTrpGlyThr 320
 Db 1114 ACATCCCTTATGTTGGAACACAGAGGCGCAGATTCATTCCTTAAACAGGTACA 1173
 QY 321 AlaAspProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
 Db 1174 GCAAAATCTTAAAGCTCTTTTAAAGATGTCGAATAATATGATGCTGAAGGAAAGATC 1233
 QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 Db 1234 ATGATGTCTATAGATAAGAGCAATTAATTCACCTTTTGAAGTTCTATTATTTGAAGGAGTTGAA 1293

QY 361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrValaTrpSerIleLeuLeuAsp 380
 Db 1294 TATATTCGACAGCTGGATGAGCTCCTGAGGAAATATGCTTGTGCATCTACTAGTAT 1353
 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
 Db 1354 CGCTCCAGACTCGCTACAGATATGTTGATCTCACCTGAATTAATTTATCCAGTAGAA 1413
 QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
 Db 1414 GATGATTTTATGGAAGGCGAGACATCATTTGATGACTGCTGATTTGTGACCCCACTA 1473
 QY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
 Db 1474 ATTATCTATGAAGAAACACAGACATCTGATTAATATCCATGACATCTTTCATGTTT 1533
 QY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysTyrHisGlyPhe 460
 Db 1534 CCCAAAGTCACGAAAGGAAATTTGACTTATTTTCCCTGATGCCAAACAGGTTTC 1593
 QY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
 Db 1594 CGTCATTTATACAAATTAATCATCTATTTAAGGAAAGCAATTAACCATCCAGTGT 1653
 QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
 Db 1654 GGGTGCTGCTCCAAAGTGAATTCATCAAGTGCCTATCAAGAGGAGATAGCAATTACAGT 1713
 QY 501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValaArgGluValaArg 520
 Db 1714 GGTGAATGGAGAACTTCTTGGCCGCGCATGATTAATGCCAAGTTGATGAAGTCAGAA 1773
 QY 521 LeuValTyrPheGluGluThrThrLysAspSerProLeuLysHisLeuTyrValaSer 540
 Db 1774 CTGGTATATTTTGAAGGACACCAAGACTCCCTTTAGACATCACTGTACGTAGTACT 1833
 QY 541 TyrValAsnProGlyGluValThrArgLeuThrAspArgLysTrpSerHisSerCysCys 560
 Db 1834 TACGTAATCTCGGAGAGGAGGACAAAGCTGACGACCGGTACCTCACATTTCTGTCC 1893
 QY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
 Db 1894 ATCAGTCAGACCTGTGACTTCTTTATAGTAAGTATGTAACCAAGAAATCCACACTGT 1953
 QY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysTrpHisGluPhe 600
 Db 1954 GTGTCCCTTTACAAAGCTATGAAGCTCTGAAGATGACCCAACTTGCAAAACAGAAATTT 2013
 QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
 Db 2014 TGGGCCACCATTTTGGATTCAGACGAGTCTCTCTGACTATATCTCCAGAAATTTTC 2073
 QY 621 SerPheGluSerThrThrArgLysPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
 Db 2074 TCTTTTGAAGTACTACTGGAATTTTACATTTATGATGATGCTCTACAGCTCAAGACTA 2133
 QY 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGly--ProGlnValGln 660
 Db 2134 CAGCTTGAAAGAAATATCTCTACTGTCTGCTCATATATGTGTGTCTCTCAGCTGCACT 2193
 QY 660 euValaAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuG 680
 Db 2194 TGGGATTAATCGGTAAAGGAGTCAAGATATTTCCGCTTGAATACCTTAGCCCTCTAG 2253
 QY 680 LysTyrValValaValaIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluG 700
 Db 2254 GTTATGTGTGATGATGATGATGACAAACAGGGAGTCTCTCAACCGAGGCTTAAATTTGAAG 2213
 QY 700 LysAlaPheLysTyrLysMetGlyGlnIleGluIleAspArgGlnValaGlyLysGln 720
 Db 2314 GCGCTTAAATATTAATAATGCTCAATATGAATATGACATGACAGTGAAGGACTCCAAT 2373
 QY 720 yLeuAlaSerArgTyrAspPheIleAspLeuAspArgValaGlyIleHisGlyTrpSer 740

Db	2374	ATCTAGCTTCTCGATATGATTTTCATTGACTTGTGATCGTGTGGCATCCAGGGCTGGTCT	2433
Oy	740	YTGILGILYTYIleuSerIleuMetGlnArgSerAspIlePheArgValAlaI	760
Db	2434	ATGGAGGATACCTCCCTCCGATGCATTAATCCAGAGGTCAAGATATCTTCAGGGTTGCTA	2493
Oy	760	IeAlaGILValArgValThrIleuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrM	780
Db	2494	TTGGCTGGGGGCCCACTCACTCTGTGGATCTTTATGATACAGATACAGCGAACGTTATA	2553
Oy	780	eGILYHisProAspGlnAsnGluGlnGlyTyrTYTYTYLeuGlySerValAlaMetGlnAlaG	800
Db	2554	TGGGTACCCCTTACCCAGATGAACAGGGCTATTACTTAGAGTCTGGCCCATGCAAGCAG	2613
Oy	800	IuLYPheProSerGluProAsnArgLeuIleuIleuHisGlyPheLeuAspGluAsnV	820
Db	2614	AAAGATCTCCCTTACCAACCAAAATCGTTTATCTCTTACATGATGTTCCGATGAGAAAG	2673
Oy	820	AlHisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrA	840
Db	2674	TCCATTTTGGACATACAGAGTATATTACTGAGTTTTTTACTGAGGGCTGGAAAGCCATAG	2733
Oy	840	sPLeuGlnIleYrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisT	860
Db	2734	ATTTCACAGTCTATCTCTCAGGAGAACACAGCATAAAGACTTCTCGAATGGGAGAACATT	2793
Oy	860	YrGILeuHisIleuLeuHisTYTYTYLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuT	880
Db	2794	ATGACATCGATCTTTTGGACACTACCTTCAAGAAACCTTGGATCAGGTATTGGTGGCTTAA	2853
Oy	880	ysValIle 882	
Db	2854	AAAGTATA 2861	
RESULT 8			
ABK83332			
ID	ABK83332	standard; CDNA. 4685 BP.	
XX	ABK83332:		
XX	12-AUG-2002 (first entry)		
DE	CDNA encoding human DPRP-1 splice variant #8.		
XX	Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;		
KW	DPRIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;		
KW	diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;		
KW	heart failure; hypertension; urinary retention; osteoporosis; cancer;		
KW	ulcer; allergy; cancer; psychotic disorder; neurological disorder;		
KW	dyskinesia; reproductive disorder; inflammatory disorder;		
KW	metabolic disorder; gene; ss.		
XX	Homo sapiens.		
OS	MO200231134-A2.		
PN	18-APR-2002.		
XX	12-OCT-2001; 2001WO-US31874.		
XX	12-OCT-2000; 2000US-240117P.		
XX	(FERR) FERRING BV.		
XX	Qi S, Akinsanya KO, Riviere PJ, Junten J;		
XX	WPI; 2002-444178/47.		
XX	P-PSDB; ABG61601.		
XX	New dipeptidyl peptidase IV-related proteins and nucleic acids encoding		
XX	the proteins, useful for treating e.g. fungal, bacterial, protozoan and		
XX	viral infections, cancers, allergies, neurological disorders, or pain		

xx	-	
pt	Disclosure: Page 75-76; 113pp; English.	
ps		
cc	The present invention relates to the isolation of novel human serine	
cc	proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related	
cc	proteins (DPP). The dipeptidyl peptidase IV-related proteins (DPP)	
cc	and nucleic acids encoding them are useful for treating infections	
cc	such as fungal, bacterial, protozoan and viral infections, particular	
cc	infections caused by human immunodeficiency virus (HIV-1 or HIV-2),	
cc	pain, diabetes, precocious puberty, infertility, obesity, anorexia,	
cc	bulimia, Parkinson's disease, acute heart failure, hypotension,	
cc	hypertension, urinary retention, osteoporosis, angina pectoris,	
cc	stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,	
cc	psychotic and neurological disorders (e.g. anxiety, dementia, or	
cc	schizophrenia), and dyskinestias. These may also be used in discovering	
cc	therapeutic agents for the treatment of reproductive, inflammatory and	
cc	metabolic disorders. ABK03322-ABK83343 encode human DPP proteins.	
xx		
sq	Sequence 4685 BP; 1430 A; 853 C; 991 G; 1411 T; 0 other;	
	Alignment Scores:	
	Pred. No.: 0 Length: 4685	
	Score: 4385.50 Matches: 834	
	Percent Similarity: 94.56% Conservative: 0	
	Best Local Similarity: 94.56% Mismatches: 1	
	Query Match: 93.31% Indels: 48	
	DB: 24 Gaps: 1	
	US-10-070-464-1 (1-882) x ABK03332 (1-4685)	
qy	1 Metalaalaamketglutrhrglunleuglyvalglutlephcglutrhlaaspys 20	
db	214 ATGGAGCAGCAATGGAAGACAGAACCTGGCTGGTTCAGATATTCGAAACCTCGGACGT 273	
qy	21 Gluglunsnlieguserrginasparcpolyseuglupropheryvaldlunrqr 40	
db	274 GAGGAGATATTGATACACAGATCGGCTTAATTGGAGCCTTTTATTTGACGGGAT 333	
qy	41 Sertrpsergineulnlyslvseuleualaaspthrarlystrhiisgllytrmetnet 60	
db	334 TCTGGAGTACGCTTAAAGAGCTGCTGCCGATACCAAGAAATATCATGCTACATGATG 393	
qy	61 AlalysaliaprohisasprhmetphevallysargAsnaspproaspolyprhiiser 80	
db	394 GCTAAGGACCAACATGATTCATGTTGTAAAGAGAAATGATTCACATGAGACTTATCA 453	
qy	81 Aspargliletryrrleualaametserrglvluasnargluasnthreuphetyrser 100	
db	454 GACAGAAATCTTATACCTTCCCATGCTCGGAGAACAGAGAAATACATGTTTATCT 513	
qy	101 GlutlepolysrthrlleasnargalalaValleumetleusertrplysProleu 120	
db	514 GAAATTCGCAAAACTATCAATATAGAGCAGCTGTATATGCTCTCTTGGAGGCTCTTTTG 573	
qy	121 Aspleuphegnialatrhrlleaspyrlyglmetlyserargglunleu 140	
db	574 GATCTTTTTCAGGACACACTGACATATGATATTTCTCGAGACAGAACTATTAGA 633	
qy	141 GluutrglysarlyleglythrvalglylealeaSertryAsptyrhiisnlysergly 160	
db	634 GAAAGAAAACCATTTGAGACAGTGGAAATGCTTCTTACGATTTATCCACAAGAGATGA 693	
qy	161 Threpleuphegnialaiglyserglylletyrrhiisvallylaspsolylylproclngly 180	
db	694 ACATTTCGTTTCAAGCGCGGATGAGATTTATTCACGTAAAGATGAGGCGCACAGGA 753	
qy	181 PhertrnglninProleuargproasleuValgluthsercysproasnleargmet 200	
db	754 TTTACGACACACTTTTAAGGCCAATCTATGTGAAGAACTAGTTGCCACACTAGGATG 813	
qy	201 Aspprolyseuysproalaaspproasptprilealaphnelhisserasnspile 220	

D8 814 GATCCAAATTTATGCGCTGCTGATCCAGACTGATGCTTTTATACATACAGACATATT 873
QY 221 TTPILeserAinileValThrArgGluGluArgArgLeuThrTyValHisAsnGluLeu 240
D8 874 TGGATATCTAACATCGTAAACAGAGAAAGAGACGCTACTATGTCACATAGCTA 933
QY 241 AAlasmetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGlu 260
D8 934 GCCAACATGAGAGAGATGCCAGATCAGCTGAGTCCCTCTGCTCCAAAGAGAA 993
QY 261 PheAspArgTySerGlyTyThrTrpCysProLysAlaGluThrThrProSerGly 280
D8 994 TTTGATGATATTTCTGCTATTGCTGCTGCTCCAAAGCTGAACACTCCAGTGGT 1053
QY 281 LysIleLeuArgIleLeuTyGluGluAsnAspGluSerGluValGluIleIleHisVal 300
D8 1054 AAAATTTCTAGAAATCTATATGAGAAATGTAATCTGAGGCTGAATTTATTCATGTT 1113
QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyProLysThrGlyThr 320
D8 1114 ACATCCCTATGTTGGAAACAGAGGCGACATTCATTCCTGTTATCTAAACAGCTACA 1173
QY 321 AAlasProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
D8 1174 GCAAATCTTAAAGTCACCTTTTAAAGATGTCAGAAATAAATGATTGATGTCGAAGAAAGATC 1233
QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
D8 1234 ATAGATGTCATAGATAAGCAATCAATCACTTTGATTCATTTGAAGAGACTTGA 1293
QY 361 TyrIleAlaArgIleGlyTrpThrProGluGlyLysTyraIleTrpSerIleLeuLeuAsp 380
D8 1294 TATATGGCAAGCTGGATGAGCTCTGAGGAAATATGCTGGTCCATCTACTAGAT 1353
QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProAlaGlu 400
D8 1354 CGCTCCCGACGATCCGCTACATATGATGTCATCTGAAATTAATTAATCCCACTAGA 1413
QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
D8 1414 GATGATGTTATGAAAGGACAGACATCATGATGATGCGCTGATGCTGACGCGCACTA 1473
QY 421 IleIleTyGluGluThrThrAspIleIleTrpIleAsnIleHisAspIlePheHisValPhe 440
D8 1474 ATTATCTATGAGAAACAACAGACATCTGATTAATATCATGACATCTTCACTGTTTTT 1533
QY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
D8 1534 CCCCAAGATCCAGAGAGAGAAATGAGTTTTATTTTGCCTGGAATGCAAAACAGGTTTC 1593
QY 461 ArgHisLeuTyTyLysIleThrSerIleLeuLysGluSerLysTyLysArgSerSerGly 480
D8 1594 CGTCATTTATACAAATATACATATATTAAAGGAACCAATATAACGATCCAGTGCT 1653
QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
D8 1654 GGGCTGCTGCTCCAGAGATTTCAAGTCTCTATCAAAAGAGAGATGCAATTCACGAT 1713
QY 501 GlyLysLysProGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
D8 1714 GGTGAATGGGAAGTCTTGGCGCGCATGATCTAATATCCAAAGTTGATGAAGTCCGAAGG 1773
QY 521 LeuValTyPheGluGlyThrLysAspSerProLeuGlnHisIleLeuTyValValSer 540
D8 1774 CTGGATATTTTGAAGGACCAAGACTCCCTTAGAGCATCACTCTAGCTAGTACTGAT 1833
QY 541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTySerHisSerCysCys 560
D8 1834 TACGTAATCTCTGGAGAGTGAAGCTGACTGACCTGCTACTCTCAATCTTCTGCTGCGC 1893
QY 561 IleSerGlnHisCysAspPheIleSerLysTySerAsnGlnLysAspProHisCys 580
D8 1894 ATCACTGACGACTGACTTCTTATAGTAAGTATAGTAAACCAAGAAATCCACACTGCT 1953

QY 581 ValSerLeuTyTyLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
D8 1954 GGTCTCCCTTTACAACCTATCAAGTCTCTGAGATGACCCCAACTGTGCAAAACAGAAATTT 2013
QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyThrProProGluIlePhe 620
D8 2014 TGGCGCACCATTTTGGATTCAGT----- 2036
QY 621 SerPheGluSerThrThrGlyPheThrLeuTyGlyMetLeuTyLysProHisAspLeu 640
D8 2036 ----- 2036
QY 641 GlnProGlyLysTyProThrValLeuPheIleTyGlyGlyProGlnValGlnLeu 660
D8 2037 -----CCTCAGGTCGAGTTG 2051
QY 661 ValAsnAsnArgPheLysGlyValLysTyPheArgLeuAsnThrLeuAlaSerLeuGly 680
D8 2052 GTGAATTAATCGGTTTAAAGAGACTCAAGTATTTCCCTGAAATACCTAGCCTCTAGCT 2111
QY 681 TyrValValValValIleAspAsnArgLysSerCysHisArgGlyLeuLysPheGluGly 700
D8 2112 TATGTGTTGTATGATAGACACAGGGATCTCTGACCGAGGCGCTTAAATTTGAAGGC 2171
QY 701 AlaPheLysTyTyLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTy 720
D8 2172 GCCTTTAATATATAATATGGTCAATAGCAATTTGACGATCAGCTGAGAGACTCCAAATAT 2231
QY 721 LeuAlaSerArgTyAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTy 740
D8 2232 CTAGCTCTCGATATGATATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2291
QY 741 GlyLysTyTyLysSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
D8 2292 GGAGATACCTCTCCCTGATGCGATTAATGACAGAGCTGAGATATCTTCAAGGTTCTAT 2351
QY 761 AlaGlyAlaProValThrLeuTrpIlePheTyraTrpThrGlyTyThrGluArgTyMet 780
D8 2352 GCTGGGGCCCGAGTCACTGCTGATCTTTATGATACAGGATACAGGAAAGCTTATATG 2411
QY 781 GlyHisProAspGlnAsnGluGlnGlyTyTyLysGlySerValAlaMetGlnAlaGlu 800
D8 2412 GGTCACTCCCTGACAGAAATGACAGGCTTATCTTAGATGATCTGTGGCATGCAACAGAA 2471
QY 801 LysPheProSerGluProAsnArgLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
D8 2472 AAGTTCCTCTGAACCAAAATGTTTACTGCTTACATGATGTTTCTGATGATGATGCTC 2531
QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyArg 840
D8 2532 CATTTTGCATACAGCATATATCTAGAGTTTATAGTAGAGGCGTGGAAAGCATATGAT 2591
QY 841 LeuGlnIleTyProGlnGluArgHisSerIleArgValProGluSerGlyCysIleTy 860
D8 2592 TTACAGATCTATCCCTCAGAGAGACACAGCATAAAGAGTTCCGTAATCCGGAGAACATTA 2651
QY 861 GlyLeuHisLeuLeuHisTyTyLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
D8 2652 GAAGTCACTTTTTCCTACTTACTTCAAGAAACCTTGGATCAGTATGCTGCTCTAA 2711
QY 881 ValIle 882
D8 2712 GTGATA 2717
RESULT 9
ABK83331
ID ABK83331 standard; cDNA: 4676 BP.
AC ABK83331:
XX
XX 12-AUG-2002 (first entry)
XX

DE cDNA encoding human DPRP-1 splice variant #7.
 XX Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 XX DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychiatric disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200231134-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US31874.
 XX
 PR 12-OCT-2000; 2000US-240117P.
 XX
 PA (FERR) FERRING BV.
 XX
 PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
 XX
 DR WPI: 2002-444178/47.
 DR P-PSDB: AB661600.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT viral infections, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT
 XX
 PS Disclosure: Page 72-73; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotropic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABR83322-ABR83343 encode human DPRP proteins.
 CC
 XX
 SQ Sequence 4676 BP; 1424 A; 859 C; 979 G; 1414 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 4676
 Score: 4385.00 Matches: 831
 Percent Similarity: 94.22% Conservatve: 0
 Best Local Similarity: 94.22% Mismatches: 1
 Query Match: 93.30% Indels: 51
 DB: 24 Gaps: 1
 US-10-070-464-1 (1-882) x ABR83331 (1-4676)
 OY 1 MetAlaAlaAlaMetGluThrGluGluGluValGluIlePheGluThrAlaAspCys 20
 DB 214 ATGCGACGACGATGGAACACAGACAGCTGGCTTGAATATTGAACTGCGACTGT 273
 OY 21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
 DB 274 GAGGAAATATTGAATCACAGGATCGGCTAAATGTGAGGCTTTATGTGAGCGGTAT 333
 OY 41 SerTyrSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
 DB 334 TCCGTGAGTCAGCTTAAAAAGCTGCTTGGCGATACCAAGAAATATATCATGCTACATGATG 393

OY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspLysProHisSer 80
 DB 394 GCTAAGCCACCAATCATATTTCATGTTGTGAAGAGAAATGATCCACATGACCTCATTTCA 453
 OY 81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
 DB 454 GACAGATCATATTAATCACTCCATCTGCTGTGAGAACAGAAATACACTGTTTATATCT 513
 OY 101 GlnIleProLysThrIleAsnArgAlaAlaValIleMetLeuSerTyrPheProLeuLeu 120
 DB 514 GAAATTCACCAAACTATATCAATAGACGACGACTTATATCTCTTGGAAAGCTCTTTTG 573
 OY 121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuAsnArg 140
 DB 574 GATCTTTTCAGGACCACTGGACTGATGGAATGTATTCGAGAACACACATTAAGA 633
 OY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
 DB 634 GAAAGAAAACGCAATGGAACAGTCGGAATTCCTTACGATTTATCCACAGAACTGGA 693
 OY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspLysLysProGlnGly 180
 DB 694 ACAATTCGTGTTCAAGCCCGTAGTGGAAATTTATACACTTAAAGATGAGGCGCACAGA 753
 OY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
 DB 754 TTACGCCAACACCTTAAAGGCCCATCTAGTGAACATAGTTGCCAACATACGAGAT 813
 OY 201 AspProLysLeuLysProAlaAspProAspTyrPheAlaPheIleHisSerAsnAlle 220
 DB 814 GATCCAAAATATATGACCTGCTGATCCAGACTGATGCTTATATATATGCAACGATAT 873
 OY 221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
 DB 874 TGATATCTTAACATCTTAACACAGAGAGAGAGACTCATTTATGCAATGACGTA 933
 OY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
 DB 934 GCCAATCATGAAAGAAATGCCAGATCAGCTGAGTGGTCTTGTCTCCACAGAA 993
 OY 261 PheAspArgTyrSerLysIleTyrTrpCysProLysAlaGluThrProSerGlyGly 280
 DB 994 TTGTGATGATATTTCTGCTATGCTGCTGCTCCAAAGCTGAACCACTCCAGTGTGT 1053
 OY 281 LysIleLeuArgIleLeuLysGluGluAsnAspLysSerGluValGluIleIleHisVal 300
 DB 1054 AAATTTCTTAAGATTTCTATATGAGAAATGATGATTCGAGGTGAATTTATCTATGTT 1113
 OY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
 DB 1114 ACATCCCTATATGTTGAAACCAAGAGGAGATTCATTCCTGTTATCTTAAACAGGTACA 1173
 OY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgTyr 340
 DB 1174 GCNAATCTTAATCTCACTTTTAAGATGTCAGAAATATATGATTCCTGAAGACAGATC 1233
 OY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 DB 1234 ATGATGTCATAGATATAGAGACTAATTCACACTTTTGAGATTTATTTGACAGAGTTGAA 1293
 OY 361 TyrIleAlaArgAlaGlyTyrThrProGluGlyLysTyrAlaTyrSerIleLeuLeuAsp 380
 DB 1294 TATATTTGCCAGACTGATGAGACTCTTGAGGGAATATGCTTGCCATCTCACTAGAT 1353
 OY 381 ArgSerGlnThrArgLeuGlnIleValIleLeuIleSerProGluLeuPheIleProValGlu 400
 DB 1354 CGCTCCACAGCTCCCTAAGATATGTTGATCTCACTCACTGAATATTTATCCAGTAGAA 1413
 OY 401 AspAspValMetGluArgGlnArgGluIleGluSerValProAspSerValThrProLeu 420
 DB 1414 GATGATGTTATGGAAGAGAGAGACTCATTTGAGTCACTGCTGATTTCTGTGAGCCACACTA 1473
 OY 421 IleIleTyrGluGluThrThrAspIleTyrPheAsnIleHisAspIlePheHisValPhe 440

Db	1474	ATTATCTATGACAAACACACACACTCTGGATTAATATCCATGACACTTTTCATGTTTTT	1533
Qy	441	ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe	460
Db	1534	CCCCAAGTCACGAAGAGAAATTTGAGTTTATTTTTGCCCTGGATGCAAAACAGTTTC	1593
Qy	461	ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerCely	480
Db	1594	CGTCATTTTATACAAAAATTAACATCTAATTTTAAAGGAAGCAAAATATAAACGATCCAGTG	1653
Qy	481	GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer	500
Db	1654	GGGCTGGCTCTGCCAAGTCATTTTCAAGTCTCCATTCAAAGAGAAATAGCAATTAACCGT	1713
Qy	501	GlyLysIleProGluValLeuGlyArgHisGlySerAsnIleGluValAspGluValArgArg	520
Db	1714	GGTAATAGGGAAGTCTTGTCGCCGCATGGATCAATATCCAAAGTTGATGAAGTCGAAGG	1773
Qy	521	LeuValTyrPheGluGlyThrLysAspSerProLeuGlnHisLysLeuTyrValValSer	540
Db	1774	CTGGTAATATTTTGAAGGCACCAAGACCTCCCTTTAGACATCACCTGACGTAGTCAGT	1833
Qy	541	TyrValAsnProGlyGluValIleThrAlaGluThrAspArgGlyTyrSerHisSerCys	560
Db	1834	TACGTAAATCTCGAAGGCGACAAAGGCGACTGACCGCGCTACTCACATTTCTGCTGC	1893
Qy	561	IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys	580
Db	1894	ATCAGTCACACACTGTACTCTTTATAGTAAGTATAGTAACCAACAAGATCCACACTGT	1953
Qy	581	ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe	600
Db	1954	GTGTCCTTTACAAAGCTATCAAGTACTCTGAAGATGACCCCAACTTGCAAAAGGAATTT	2013
Qy	601	TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe	620
Db	2014	TGGCCACCAATTTGGATTTGACGAGGTCTCTCCGATATACCTCCACGAATTTTC	2073
Qy	621	SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu	640
Db	2074	TCTTTGAAGTACTACTGATTTACATTTGTATGGAGATCTCTACAAAGCTCATGATCTA	2133
Qy	641	GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyLysProGlnValGlnLeu	660
Db	2134	CAGCTCGAAGAAATATCTACTGTGCGTTCATATAGCGTGGCG-----	2180
Qy	661	ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly	680
Db	2180	-----	2180
Qy	681	TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly	700
Db	2180	-----	2180
Qy	701	AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGlyGlyLeuGlnTyr	720
Db	2181	-----	2222
Qy	721	LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTyrPheTyr	740
Db	2223	CTACCTTCTCGAATATGATTTCAATTGACTTAAGATCGTGTGGCATCCACGCTGCTCAT	2282
Qy	741	GlyLysIleLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle	760
Db	2283	GGAGGATACCTCTCCCTCGATGGGATTTAAAGCAGAGTCAGATATCTTAGGGTTGCTATT	2342
Qy	761	AlaGlyAlaProValThrLeuThrIlePheTyrAspThrGlnTyrThrGlnArgTyrMet	780
Db	2343	GCCTGGGCCCCAGTCACTGTGTGATCTTCTATGATACAGATACACGGAACGTTATATG	2402
Qy	781	GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu	800

Dd	2403	GGTCAACCTTGACACGAAATGAACAGGGCTATTACTTAGAGATCTGTGGCCATGCACAAACGAA	2462
Oy	801	LysPheProSerGluProAsnArgLeuLeuLeuLeuLnisgLyPheLeuASpGIuAsnVal	820
Dd	2463	AAGTTCCCCCTCGAACAACCATCGTTTACTGTCCTTACATGGTTTTCCCGAATGAGAATGTC	2522
Oy	821	HISPhelaIalHisThrSerTlleLeuLeuSerPheLeuValAlaGlaGlyLysProTyraSP	840
Dd	2523	CATTTCGACATACACAGTAATATTACTGATGTTTTTACGAGCGCTGGAAAGCCCATATGAT	2582
Oy	841	LeugInIIleTyrrProGlnGluArgHniserTleArGylalProGlnusergLyLnHisTyrr	860
Dd	2583	TTCACGATCTATCCTCCAGAGACAGACAGCATAAAGACTCTGTAAATCGGGGAACATTTAT	2642
Oy	861	GluLeuHnIsleuLeuHnIsTyrrLeuGlnLysnLeuGlyserfArgIeAlaLeuLys	880
Dd	2643	GAACTGCAATCTTTTCCSCATACCTTCACAAACACTTGGATCACGATATTGCTGCTATAAA	2702
Oy	881	Vallile 882 	
Dd	2703	GTGATA 2708	
RESULT 10			
ID	ABNS9774		
XX	ABNS9774	standard; cDNA: 2842 BP.	
AC	ABNS9774:		
XX			
DT	28-JUN-2002	(first entry)	
DE			
XX			
XX			
KW	Human; antihaememic; vulnerability; antinflammatory; immunomodulator;		
KM	antiferility; cerebroprotective; cyclostatic; rheumatic; gene therapy;		
KN	neuroprotective; antiparkinsonian; protein therapy; EST;		
XX	expressed sequence tag; gene: ss.		
OS	Homo sapiens.		
PM	WO200222660-A2.		
PD	21-MAR-2002.		
XX			
PF	10-SEP-2001; 2001WO-US26015.		
PR	11-SEP-2000; 2000US-0659671.		
PA	(HXSE-) HXSEQ INC.		
PI	Tang Y.T., Liu C., Zhou P., Asundi V., Zhang J., Zhao Q.A., Ren F.;		
PI	Xue A.J., Yang Y., Wehrman T., Drmanac RT;		
XX	WPI: 2002-292408/33.		
DR	P-PsDB: ABB97361.		
XX			
PT	An isolated polynucleotide for treating diseases associated with its		
PT	encoded polypeptide such as cancer and multiple sclerosis -		
PS	Claim 1; SEQ ID NO 185; 509pp: English.		
XX			
CC	The present invention provides the protein and coding sequences of 444		
CC	novel human proteins. These were isolated from expressed sequences tags		
CC	(ESTs). They can be used to stimulate cell growth, to regulate		
CC	haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth		
CC	e.g. in burn treatment, to regulate the immune system e.g. to treat		
CC	multiple sclerosis, to regulate activin or inhibin e.g. to treat		
CC	fertility, to regulate haemostasis or thrombolysis e.g. to treat		
CC	stroke and cancer, to screen for drugs, to treat inflammatory conditions		
CC	e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.		
CC	Parkinson's disease. The present sequence is a coding sequence of the		
XX	invention.		
XX			
XX	Sequence 2842 BP: 857 A: 592 C: 635 G: 758 T: 0 other:		

Alignment Scores:

Pred. No.:	0	Length:	2842
Score:	4118.00	Matches:	782
Percent Similarity:	88.66%	Conservative:	0
Best Local Similarity:	88.66%	Mismatches:	100
Query Match:	87.62%	Indels:	1
DB:	24	Gaps:	1

US-10-070-464-1 (1-882) x ABNS9774 (1-2842)

QY 1 MetAlaAlaMetGluThrGluInLeuGlyAluLeuPheGluThrAlaAspCys 20
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 DB 234 ATGGACACCAATGAAAGAAAGAAACAGCTGGCTGTGATATTGTAACACGCGACTGT 293
 |||||
 QY 21 GluInLeuInLeuSerGluInAspArgProLysLeuGluProPheTyValGluArgTyr 40
 |||||
 DB 294 GAGGAGAAATTGATACAGGATCGGCTTAATTGGAGCCCTTTTATGTTGACGGGTAT 353
 |||||
 QY 41 SerTrpSerGluInLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
 |||||
 DB 354 TCCGTGAGTCAGCTTAAAGAGCTGCTGGCATACAGAAATATCATGGCTACATGATG 413
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 QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
 |||||
 DB 414 GCTAAGGACCCACATGATTTTCATGTTGTGAAGAGAAATGATCCAGATGAGCCCTATCA 473
 |||||
 QY 81 AspArgLysTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
 |||||
 DB 474 GACAGAACTATTACCTTCCCATCTGCTGAGACAGAGAAATACACTGTTTATCTT 533
 |||||
 QY 101 GluInLeuProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTyrPlyProLeuLeu 120
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 DB 534 GAATTCCTCCAAACTATCATATAGAGCAGCAGCTTAAATGCTCTCTGGAAGCCCTTTTG 593
 |||||
 QY 121 AspleuPheGluInAlaThrLeuAspTyrGlyMetTyrSerArgGluGluInLeuLeuArg 140
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 DB 594 GATCTTTTTCAGGACACAGCTGAGTATGAAATTCATCTCGAGAAGAAATCATTTTAGA 653
 |||||
 QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
 |||||
 DB 654 GAAGAAGAAAGCATTTGAGACAGCTGGAAATGCTTTCATACATTTTCACCAAGAAAGTGA 713
 |||||
 QY 161 ThrPheLeuPheGluInAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
 |||||
 DB 714 ACATTTCTGTTTCAAGCCGATGAGATTAATCAGCTTAAAGATGAGGGCCCAAGAGA 773
 |||||
 QY 181 PheThrGlnGluProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
 |||||
 DB 774 TTTCAGCAACACCTTTAAGGCCCAATCTAGTGAACCTAGTGTCCCAACATACGGATG 833
 |||||
 QY 201 AspProLysLeuCysProAlaAspProAspTyrIleAlaPheIleHisSerAspIle 220
 |||||
 DB 834 GATCCAAATATTATCCCTGCGATCCAGACGATGCTGCTTTATATACATAGCAAGATATT 893
 |||||
 QY 221 TrpIleSerAsnIleValIleThrArgGluGluArgGlyLeuThrTyrValHisAsnGluLeu 240
 |||||
 DB 894 TGGTATCTACATCTTACACAGAGAAAGAAAGAGACTCATTTATGTGCAAAATGACCTA 953
 |||||
 QY 241 AlaAsnMetGluInAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGlu 260
 |||||
 DB 954 GCCAACATGGAAGAGATGCCAGATCAGCTGAGTCCCTGTTGTTCTCCAAAGAA 1013
 |||||
 QY 261 PheAspArgTyrSerGlyTyrTrpTyrCysProLysAlaGluThrThrProSerGlyGly 280
 |||||
 DB 1014 TTTCATGATGATATTCTGCTATTGCTGCTGCCAAACCTGAAACAACTCCAGAGTGCT 1073
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 QY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
 |||||
 DB 1074 AAAATTCCTGAAATTCATATGAAAGAAATGATGAACTCTGAGTGGAATATTATCATGTT 1133
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 QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
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DB 1134 ACATCCCTATGTTGGAACAGAGCGAGATTCATCCGTTATCCCTAAACAGGTACA 1193
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 QY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluArgIle 340
 |||||
 DB 1194 GCATATCTTAAAGTCACTTTTAAAGATCTCGAATAATATGATTGCTGAGAGAGATC 1253
 |||||
 QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 |||||
 DB 1254 ATGATGTCTATGATAGAAAGAAATCAACCTTTGATGATTCATTTGAAAGAGGTGAA 1313
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 QY 361 TyrIleAlaArgAlaGlyTyrThrProGluGlyLysTyrTrpAlaTrpSerIleLeuLeuAsp 380
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 DB 1314 TATATTGCCAGAGCTGGATGAGTCCCTGAGGAAATATGCTTGCTCATCTACTAGAT 1373
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 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
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 DB 1374 CGCTCCAGACTGCGCTACAGATAGTGTGATCTCACCCTGAATATTATCCAGGTGAA 1433
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 QY 401 AspAspValMetGluArgGluArgLeuIleGluSerValProAspSerValThrProLeu 420
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 DB 1434 GATGATGTATGMAAGCAGAGACTCATGAGTCACTGCTGATCTGTGAGCGCCACTA 1493
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 QY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
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 DB 1494 ATTATCTATGAGAAACACACAGACATCGATTAATATCCATGACATCTTTCATGTTT 1553
 |||||
 QY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
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 DB 1554 CCCAAAGTCCAGAAAGAGAAATGATTTATTTTCCCTGATATCCAAACAGGTTTC 1613
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 QY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
 |||||
 DB 1614 CGTCATTTATACAAATTAATCATCTATTAAAGGAAAGCAAAATTAACATCCAGTGT 1673
 |||||
 QY 481 GlyLeuProLysProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
 |||||
 DB 1674 GGGCTGCTGCTCCAAAGTATTCCTCAAGTGTCTATCAAGAGAGATAGCAATTTACCAGT 1733
 |||||
 QY 501 GlyLeuTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArg 520
 |||||
 DB 1734 GGTAAATGGAGAGTCTTGCGCGCATGATCTAATATCCAAAGTATGAAAGTACAGAG 1793
 |||||
 QY 521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisIleLysLeuValIleSer 540
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 DB 1794 CTGGTATATTTTGAAGCACCAGCAAGCTCCCTTAAAGCATCAGCTGATAGTACGT 1853
 |||||
 QY 541 TyrValAsnProGlyGluValIleThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
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 DB 1854 TACGTAAATCTCGAGAGCGTACAGAGCTGACCTGACCTGCTACTACATTTCTTGCTGC 1913
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 QY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
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 DB 1914 ATCAGTCAGACCTGATCTTATTAAGTAAGTATGTAACAGAGAAATCCACACTGT 1973
 |||||
 QY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
 |||||
 DB 1974 GTGTCCTTTACAGGCTATACAGCTCGAAGATACCCCACTTGCAAAACAAAGAAATTT 2033
 |||||
 QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
 |||||
 DB 2034 TGGGCCACATTTTGGATTAGCAGAGTCTCTTCTTACTACTATCTCTCCAGAAATTTTC 2093
 |||||
 QY 621 SerPheGluSerThrThrArgIlePheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
 |||||
 DB 2094 TCTTTTAAAGTACTACTGATTTACATTTATAGGATGCTCTACAGGCTCATGATCTA 2153
 |||||
 QY 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
 |||||
 DB 2154 CAGCTGGAAGAAATATCTCTACTGCTGTCTCATATATGATGCTGCTCTCAG ----- 2204
 |||||
 QY 661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrIleAlaSerLeuGly 680
 |||||
 DB 2204 ----- 2204

QY 681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGlyGly
 DB 2204 ----- 2204
 QY 701 AlaPheLysTyrLysMetCylGlnIleGluIleAspAspGlnValGlnGlyLeuGlnTyr 720
 DB 2204 ----- 2204
 QY 721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTyrPheTyr 740
 DB 2204 ----- 2204
 QY 741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
 DB 2205 ----- GTTGGTATT 2213
 QY 761 AlaGlyAlaProValThrLeuThrIlePheTyrAspThrGlyTyrThrGlnArgTyrMet 780
 DB 2214 GCTGGGGCCCGACGATCTGTGATCTTCTGATACAGATACCGAGACGTTATATG 2273
 QY 781 GlyHisProAspGlnAsnGlnGlnGlnGlyTyrLeuGlySerValAlaMetGlnAlaGlu 800
 DB 2274 GGTCAACCTGACAGAAATGAACAGGGCTATTAAGATCTGTGCCATGCAAGCAGAA 2333
 QY 801 LysPheProSerGlnProAsnArgLeuLeuLeuHisGlyPheLeuAspGlnAsnVal 820
 DB 2334 AGTTTCCCTCGAACCAAAATGTTTACTGCTCTTACATAGGTTTCTGATGATGAAATGTC 2393
 QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
 DB 2394 CATTTTGGACATACCAAGATATATTAAGTCTTGTAGTAGGGCTGAAAGCCATATGAT 2453
 QY 841 LeuGlnIleTyrProGlnGlnArgHisSerIleArgValArgGlnSerGlyGlnHisTyr 860
 DB 2454 TTACAGATCTATCTCCAGAGACACAGCATAGAGTTCTGAAATCGGAGAAACATTAT 2513
 QY 861 GluLeuHisLeuLeuHisTyrLeuGlnGlnAsnLeuGlySerArgIleAlaIleLeuLys 880
 DB 2514 GAACTGCATCTTTGACACCTTCAAGAAACCTTGATGATCAGTATCTGCTCTAATA 2573
 QY 881 ValIle 882
 DB 2574 CTGATA 2579
 RESULT 11
 ABK83325
 ID ABK83325 standard; cDNA: 4523 bp.
 AC ABK83325;
 XX
 DT 12-AUG-2002 (first entry).
 XX
 DE cDNA encoding human DPP-1 splice variant #1.
 KM Human: serine protease; dipeptidyl peptidase IV-related protein; DPP;
 KM DPPIV; Infection: human immunodeficiency virus; HIV-1; HIV-2; pain;
 KM diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KM heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KM ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KM dyslexia; reproductive disorder; inflammatory disorder;
 KM metabolic disorder; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PM W0200231134-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US31874.
 XX
 PR 12-OCT-2000; 2000US-240117P.
 XX

PA (FERR) FERRING BV.
 XX
 PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
 XX
 DR WPI: 2002-444178/47.
 XX P-PSDB: ABG61594.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT
 PS Disclosure: Page 61-62; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyslexias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABK83322-ABK83343 encode human DPPR proteins.
 XX
 SO Sequence 4523 BP; 1384 A; 828 C; 940 G; 1371 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 0 Length: 4523
 Score: 4092.50 Matches: 780
 Percent Similarity: 88.44% Conservative: 0
 Best Local Similarity: 88.44% Mismatches: 1
 Query Match: 87.07% Indels: 102
 DB: 24 Gaps: 1
 US-10-070-464-1 (1-882) x ABK83325 (1-4523)
 QY 1 MetAlaAlaAlaMetGlnThrGlnGlnLeuGlyValGlnIlePheGlnThrAlaAspCys 20
 DB 214 ATGGCAGCAGCAATGCAACAGACAGCTGGGTGAGATATATGAACTGGGAGCTGT 273
 QY 21 GlnGlnAsnIleGlnSerGlnAspArgProLysLeuGlnProPheTyrValGlnArgTyr 40
 DB 274 GAGGAGAAATATTGAATCACAGATCCGCCCTAAATTCGACCTTTTATGCTTGAGCGGTAT 333
 QY 41 SerTrpSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetGln 60
 DB 334 TCCTGGAGTCAGCTTAAAGCTGCTTCCGATCCAGAAATATATGATGCTTACATGATG 393
 QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
 DB 394 GGTAAAGGCAACCATGATTTTCATGTTTGAAGAGAGAAATGATCCAGATGGAGCTCATTTCA 453
 QY 81 AspArgIleTyrTyrIleuAlaMetSerGlyGlnAsnArgGlnAsnThrLeuPheTyrSer 100
 DB 454 GACAGATATTATTAACCTTCCATGCTGTGAGAACAGAGAAATACACGTTTATTTCT 513
 QY 101 GlnIleProLysThrIleAsnArgAlaAlaValIleMetLeuSerTrpLysProLeuLeu 120
 DB 514 GAAATTCCTCAAAACTATCATATAGACAGAGATCTTATATGCTCTTGGAAAGCTCTTTTGG 573
 QY 121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGlnGlnGlnLeuLeuArg 140
 DB 574 GATCTTTTTCAGGACACACTGGACGTATGCAATGTATTTCTGAGAAAGCAAGATTAAGA 633
 QY 141 GlnArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
 DB 634 GAAAGAAACGCAATGGAGACAGTGGAAATTCCTTTACGATTTATCCACCAAGCAACTGCA 693

OY	161	ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyLysProGlnGly	180
Db	694	ACATTCTGTTTCAAGCCGGAGTGGAAATTATTCACGTAAATGAGGGCCACAGGA	753
OY	181	PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet	200
Db	754	TTTACGCAACAACCTTTTAAGGCCCAATCTAGTGGAAACTAAGTTGTCCCAACATACGAGATG	813
OY	201	AspProLysLeuCysProAlaAspProAspTyrIleAlaPheIleHisSerAsnSpIle	220
Db	814	GATCCAAAATATATGCGCTCGTGAATCCAGATGGATTGCTTTTATCATGACGAACGATATT	873
OY	221	TyrPheSerAsnIleValThrArgGluGluArgLeuThrTyrValHisAsnGluLeu	240
Db	874	TGGATATTTAACTATCGTATACCAAGAAAGAAAGAGACTCTATTATGCAATGAGCTTA	933
OY	241	AlaAsnMetGluGluAspAlaArgSerAlaGluValAlaThrPheValLeuGlnGlu	260
Db	934	GCCAACTAGGAAGAAGATGCCAGATCCAGCTGGAGTGGCTACTTTTGTCCACAGACGA	993
OY	261	PheAspArgTyrSerGlyTyrTyrPyrCysProLysAlaGluThrThrProSerGlyGly	280
Db	994	TTTGATAGATATTCCTGGCTATGTGTGGTGCACAAAGCTGAACCACTCCAGGTGTGT	105
OY	281	LysIleLeuAlaGlyIleLeuTyrGluGluAsnAspCysLeuGluIleIleHisVal	300
Db	1054	AAAAATCTTAAATTTCTATATGAAAGAAAAGAAATCTGAGGTGGAAATTTATCATGTT	1113
OY	301	ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr	320
Db	1114	ACATGCCCTATGTTGGAAACAAGAGGGCCAGATTCACTCCGTTATCTTAACAGGTACA	1177
OY	321	AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle	340
Db	1174	GCAATTCCTAAAGTCACATTTTAAGATGTCAAGAAATATATGATTGACTCGAAGGAAGATC	1233
OY	341	IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu	360
Db	1234	ATAGATGTCAATAGATTAAGAACTAATTAACCTTTTGACGATTTTATTTAAGAGAGTTGAA	1293
OY	361	TyrIleAlaArgAlaGlyTyrThrProGluGlyLysTyrIleThrSerIleLeuLeuAsp	380
Db	1294	TATATTTGCCAAGCTGGATGGAGACTCCCGAAGGAATAATCTGTGGTCATCTCACTACGAT	1355
OY	381	ArgSerGlnThrArgLeuGlnIleValLeuIleSerProIleuPheIleProValGlu	400
Db	1354	CGCTCCAGACTCGCCCTACAGATAGTGTGATGTCACTGTAATATTATTTCACAGTAGAA	1411
OY	401	AspAspValMetGluValGlnArgLeuIleGluSerValProAspSerValThrProLeu	420
Db	1414	GATGATGTTTATGGAAGAAGCGAGAGACTCATTAAGTCAAGTGGCTGATTTCTGAGCCACTA	1472
OY	421	IleIleTyrGluGluThrThrAspIleTyrPheIleAsnIleHisAspIlePheHisValPhe	440
Db	1474	ATTATCTATGAGAAACACAGACGACATGTGGATAAATATCCATGACATCTTTATGATGTTTT	1533
OY	441	ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe	460
Db	1534	CCCCAAAGTCAAGAAAGAAATTTGAATTTATTTTGGCTGTAATGCAAAACAGATTTTC	1593
OY	461	ArgHisLeuTyrLysIleIleThrSerIleLeuLysGluSerLysTyrLysArgSerGly	480
Db	1594	CGTCAATTTTACAAATTTACATCTATTTTAAAGAAAGCAAAATATTAACATGCCAGTGGT	1653
OY	481	GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleIleAlaIlePheSer	500
Db	1654	GGGGCGCTGCTCCAAAGTGAATTTCAATGTCTCATTAACAAGAGAGATTAACCAATTTACCACT	1713
OY	501	GlyLysThrGluValIleLeuGlyArgHisGlySerAsnIleGlnValAspLysValArgArg	520
Db	1714	GGTGAATGGGAAGTTCTTGTGGCCGCAAGATCTATATATGCCAAGTTGATGAATGCCAAGG	1773
OY	521	LeuValTyrPheGluGlyThrLysAspSerProLeuGlnHisIleuTyrValValSer	540

Dd	1774	CTGGTATATTTTGAAGCCACCAAGACTCCCTTTAGACATCACCTGTAGCTACTAGT	1833
Qy	541	TYRVALANPROGILGIVALLTHNARGLEUTHRASPARGLTYRSEHNISSECYSCYS	560
Dd	1834	TACGTAATCTCGAGAGGAGACAGGCTGACGACGGTGGCTACATTTCTGCTGC	1893
Qy	561	ILSERGLNHSICYSASAPRHEPHEILSERLYSTYRSASGLNLYASAPROHISYCS	580
Dd	1894	ATCATCTGACGACCTGTGACTCTTTATPAGTAATPACTAACCAAGAAATCCACACGT	1953
Qy	581	VALSERLEUTHLYLSLEUSERSEPROGLIASPASPROTHCYLYSTHLYSGLUHPE	600
Dd	1954	GTGTCCCTTTACAAGCTATGACAGTCTGAAGATGACCCAACTTGGAAACAAAGAAATTT	2013
Qy	601	TRPALATHILLEAASPSERIALAGLYPROLEUPROASPITYRTHPROGILUHLPEH	620
Dd	2014	TGGGCCACACATTTTGGATTCAGCAGGCTCCTTCCGACTAATACCTCCGAAATTTTC	2073
Qy	621	SERPHGLUSERTHRHGILYRPHETHLEUTHGLYMETLEUTHLYSPROHISASPLEU	640
Dd	2074	TCTTTTGAATTAAGTACTGATGATTTACATTTGATGAGATCTCTTAACACCTCATGATCTA	2133
Qy	641	GLNPROGLYSLYSTYRPROTHVALLEUPHEILLETYRGLYGLYPROGLINVALGLIEU	660
Dd	2134	CAGCCTGGAAAGAAATATCTTACTGTCGCTTTCATATTAAGGGGT-----	2178
Qy	661	VALASNAARGPHELYSGLYVALLYSTYRPHARGLEUASNTHEULALASERLEUGLY	680
Dd	2178	-----	2178
Qy	681	TYRVALVALVALVALLEASPASNARGGLYSERCYSNLSARGGLYLEULYSPHEGLUGLY	700
Dd	2178	-----	2178
Qy	701	ALAPHELYSTYRLYSMETGLYGLNLEGLINLEASPASGGLNVALGLYLEUGLINTYR	720
Dd	2178	-----	2178
Qy	721	LEULASERARGTYRASPHEILEASPLEASPARGLVALGLILENLSGLYTRPSEYRGT	740
Dd	2178	-----	2178
Qy	741	GLYGLYTYRLEUSERLEUMETLALAEUMETGLNARGSERASPILEPHARGVALALALLE	760
Dd	2179	-----CGGTT--GCTATT	2189
Qy	761	ALAGLYALAPROVALTHNLEUTHRIEPHETYRASPTHGLYTYRTHGLUARGTYMET	780
Dd	2190	GCTGGGGCCACGACACTGCTGGATCTCTTATGATACAGGATACAGGAACTGTTATG	2249
Qy	781	GLYNHSPROASPGILNANGLUNGINDLYTYRTYRLEUGLYSERVALALAMETGLNALAGLY	800
Dd	2250	GCTACCCCTGACCAAGATGACAGGGCTATPACTTGAATCTGTGTGGCCATGCACACGAA	2309
Qy	801	LYSPHERPROSERGLUPROASNARGLEULEULEULENHSIGLYRHELEUASPDLYASVAL	820
Dd	2310	AAGTTCCCCCTGAAACCAATCGTTTACTGCTCTTACATGAGTTTCCGTGGATGAGAACTGC	2369
Qy	821	HISPHLEALHNHSTHSERTILEULEUSERPHELEUVALARGALAGLYUSPROTYRASP	840
Dd	2370	CATTTCGACATACCACTATATPACTGAGATTTTGTAGTAGGGCTGGAAGCCATATCAT	2429
Qy	841	LEUGNILEUTHYRPROGLINGLYARGNHSISSERTIARGVALPRGILUSERGLYGLNHSTYR	860
Dd	2430	TTACAGACTATCTCTCAAGAGACACACACATPAGAGTTCTGAAATCGGGAGAACATPAT	2489
Qy	861	GLULEUHNISLEULEUHNHSTYRLEUGINDLYASNLEUGLYSERARGILEALALAEULYS	880
Dd	2490	GAACTGACATCTTTTGGACATCACTTCAAGAAACCTTGATCAACGATATGTGCTGCTTAAA	2549
Qy	881	VALILE 882	

Db 2550 GTGATA 2555

RESULT 12

AAID23843

ID AAD23843 standard; cDNA: 2510 BP.

XX AAD23843;

AC AAD23843;

XX 07-MAR-2002 (first entry)

DT Human protease PRTS-2 cDNA.

DE Human protease PRTS-2 cDNA.

XX Human; protease: PRTS-2; tranquilizer: gene therapy; vaccine; allergy;

XX Infection; dermatitis; arteriosclerosis; rheumatoid arthritis; hepatitis;

XX atherosclerosis; psoriasis; Alzheimer's disease; mental disorder; cancer;

XX gastrointestinal disorder; Cushing's syndrome; seizure; glaucoma; stroke;

XX epithelial disorder; urticaria; anorexia; trauma; asthma; eczema; nausea;

XX hypertension; neurological disorder; Parkinson's disease; drug screening;

XX cardiatic; cell proliferative disorder; multiple sclerosis; osteoporosis;

XX diabetes mellitus; glomerulonephritis; cardiovascular disorder; anaemia;

XX autoimmune disorder; inflammatory disorder; myocardial infarction; AIDS;

XX developmental disorder; reproductive disorder; infertility; diarrhoea;

XX dementia; acidosis; cataract; gynaecomastia; epilepsy; jaundice; ss.

XX Homo sapiens.

XX Location/Qualifiers

FT CDS 616..2358

FT /Page a

FT /Product- "Human protease PRTS-2 protein"

PN MO200183775-A2.

XX 08-NOV-2001.

XX 04-MAY-2001: 2001WO-US14651.

XX 04-MAY-2000: 2000US-202082P.

XX 11-MAY-2000: 2000US-203566P.

XX 17-MAY-2000: 2000US-205803P.

XX 25-MAY-2000: 2000US-207477P.

XX 01-JUN-2000: 2000US-209402P.

XX (INCY-) INCYTE GENOMICS INC.

XX Deleage AM, Lal P, Hafalia A, Patterson C, Walla NK, Kearney L;

XX Tribouley CM, Khan FA, Yao MG, Baughn MR, Azimzai Y, Elliott VS;

XX Nguyen DB, Gandhi AR, Yang J, Hernandez R, Policky JL, Lu DM;

XX Reddy R, Yue H, Tang YT;

XX WPI: 2002-034518/04.

XX P-PSDB: AAEL4337.

XX Novel human proteases and polynucleotides encoding the proteases,

XX useful for treating, diagnosing or preventing cell proliferative,

XX cardiovascular, autoimmune/inflammatory, neurological and developmental

XX disorders -

XX Claim 5: Page 139-140; 151pp: English.

XX The invention relates to human proteases (PRTS-14) and its corresponding

XX cDNA molecules. Human PRTS and its nucleic acid molecule are useful for

XX the diagnosis, treatment and prevention of disorders associated with

XX increased or decreased expression of PRTS. Examples of such disorders

XX include, cell proliferative disorders (arteriosclerosis, atherosclerosis,

XX hepatitis, psoriasis and cancers); autoimmune/inflammatory disorders

XX (AIDS, Addison's disease and cancers); autoallergic/inflammatory disorders

XX (diabetes mellitus, glomerulonephritis, multiple sclerosis, osteoporosis,

XX trauma, Grave's disease, rheumatoid arthritis, ulcerative colitis, and

XX viral, bacterial, fungal, parasitic, protozoal and helminthic

XX infections); cardiovascular disorders (myocardial infarction, ischaemic

XX heart disease and hypertension); neurological disorders (epilepsy,

XX Alzheimer's disease, Pick's disease, Huntington's disease, dementia,

CC Parkinson's disease, stroke, mental disorders including mood, anxiety

CC and seasonal affective disorder and prion diseases); gastrointestinal

CC disorders (Crohn's disease, anorexia, nausea, diarrhoea and jaundice);

CC epithelial disorders (contact dermatitis, eczema, acne vulgaris,

CC alopecia, scabies, insect bites and urticaria); reproductive disorder

CC (infertility, disruption of estrous and menstrual cycle and

CC gynaecomastia); and developmental disorders (renal tubular acidosis,

CC Cushing's syndrome, seizure disorders, congenital glaucoma and cataract).

CC PRTS DNA is also in useful is gene therapy. PRTS and its immunogenic

CC fragments are useful for screening libraries of compounds in several drug

CC screening assays. The present sequence is human protease PRTS-2 cDNA.

XX

SO Sequence 2510 BP; 777 A; 494 C; 527 G; 712 T; 0 other;

Alignment Scores:

Pred. No: 0 Length: 2510

Score: 3970.50 Matches: 764

Percent Similarity: 89.81% Conservative: 3

Best Local Similarity: 89.46% Mismatches: 5

Query Match: 84.48% Indels: 82

DB: 24 Gaps: 6

US-10-070-464-1 (1-882) x AAD23843 (1-2510)

Oy 42 TpsercInleuLysLysLeuAlaAspThrArgLysTrpHisGlyTrpMetCala 61

Db 3 TGGAGTCAGCTTAAAGAGCTGCTTGGCGATACCGAAATATCTGCGCTACATATGCT 62

Oy 62 LysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSerAsp 81

Db 63 AAGCACCACATGATTTTCATGTTGTGAAGAGAAATGATCAGATGACCTATTGAC 122

Oy 82 ArgLysTrpTrpLeuAlaMetSerGlyGluAsnArgLysAsnTrpLeuPheTrpSerGlu 101

Db 123 AGAATCTAATTAACCTTGGCATGCTGTGAAGACAGAAATATACATGTTTATTTCTGAA 182

Oy 102 IleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeuAsp 121

Db 183 ATTCCCAAAACTATCATATAGACGACAGCTTAAATGCTCTTGGAAAGCCCTTTTGAT 242

Oy 122 LeuPheGlnAlaThrLeuAspTrpGlyMetTrpSerArgGluGluLeuLeuArgGlu 141

Db 243 CTTTTCAGCAACACACGACATGATGATGATGATGATGATGATGATGATGATGATGAT 302

Oy 142 ArgLysArgLysGlyTrpValGlyIleAlaSerTrpAspTrpHisGlyTrpSerGlyThr 161

Db 303 AGAAAGCGCATTTGGAACAGTCGAAATTCCTTACATATATACCAAGAGAGAGACA 362

Oy 162 PheLeuPheGlnAlaGlySerGlyIleTrpHisValLysAspGlyGlyProGluGlyPhe 181

Db 363 TTTCCTGTTTCAAGCCGCTAGTGAATTTATTCACCTAAAGATGAGAGGCCCAAGATTT 422

Oy 182 ThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMetAsp 201

Db 423 ACCGAAACACTTTAAAGCCCAATCTAGTGAAGATGTTTCCCAACATACGATGAT 482

Oy 202 ProLysLeuGlyProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIleTrp 221

Db 483 CCAAAATTAATGCTGCTGCTGATGACAGCTGATTCCTTTTATACATACCAAGATATTTGG 542

Oy 222 IleSerAsnIleValThrArgGluGluArgArgLeuThrTrpValHisAsnGluLeuAla 241

Db 543 ATATCTACATCGTAACACAGAGAAAGAGAGACTCTTATGTGCAATGACCTAGCC 602

Oy 242 AsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGluGluPhe 261

Db 603 AACATGGAAGAGATGACAGATGAGTGGAGTGGCTTGTTCACCAAGAGATTT 662

Oy 262 AspArgGlySerGlyTrpTrpTrpCysProLysAlaGluThrTrpProSerGlyGlyLys 281

Db 663 GATGATATTTCTGCTTATTTGCTGTGTGTCAAAACCTGAAACATCCCATGCTGCTAAA 722

Oy 282 IleLeuArgIleLeuValTrpGluGluAsnAspCysLeuValGluIleIleHisValThr 301

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|||||
Db 723 ATTCTAGAAATTCATATGAAAGAAAATGATGATGAGTGAAGAAATATTCAGTTACA 782
Oy 302 SerProMetLeuGluThrArg-ArgAlaAspSerPheArgTyrProLysThrGlyThrAl 321
Db 783 TCCTCTATGTTGGAAACAGGACGAGATTCATCCGTTATCCCTAAACAGGACGAC 842
Oy 321 aasnProLysValThrPheLysMetSerGluLeuMetIleAspAlaGluGlyIleI 341
Db 843 AAATCCCTAAAGTCACTTTAAGATGTCGAAATATATGATTCGTGAGAGAGATGAT 902
Oy 341 easnValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGly 361
Db 903 AGAGTCTATAGATAGGAACTCAATTCACCTTTGAGATTCATTTTGAAGAGATTGAATA 962
Oy 361 rIleAlaIleArgAlaGlyThrProGluGlyLysTyrAlaIlePheSerIleLeuLeuAsp 381
Db 963 TATTGCCAGACTGGATGGATCCTGAGGAAATATGCTTGTCATCTACTAGATCG 1022
Oy 381 gSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGluAs 401
Db 1203 CTCCAGACGCTGCTACAGATAGTGTGATCTCACTCAATATTTATCCAGATGAGA 1082
Oy 401 pasValMetLeuArgGlnArgLeuIleGlnSerValProAspSerValThrProLeuI 421
Db 1083 TGAGTTATGGAAGGACGACATCTAGTACGCTGATCTGTGAGCGCCACTAAT 1142
Oy 421 eIleTyrGluGluThrThrAspIleThrIleAsnIleHisAspIlePheHisValPhePr 441
Db 1143 TATCTATGAACAAACACACAGCATCTGATTAATATCCATGATCTTTCATGTTTCC 1202
Oy 441 oGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPheAr 461
Db 1203 CCAAGTCCAGCAAGAGAAATGATGATTATTTTGCCTGCTGAATGCAAAACAGGTTCCG 1262
Oy 461 gHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysAspSerSerGlyGl 481
Db 1263 TCATTTATACAAATATACATCTATTTTAAAGAAACAAATATTAACATCCAGTGGGG 1322
Oy 481 yLeuProLapProSerAspPheLysCysProIleLysGluLeuIleAlaIleThrSerGl 501
Db 1323 GCTGCTGCTCCACT-----GTCACI----- 1344
Oy 501 yGluThrPglVal-----LeuGly-----ArgH 509
Db 1345 ----TGGATGATCATCATGAGATCTCTAGGAATCATCTGATGTCGACACA 1400
Oy 509 sGlySerAsnIleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAs 529
Db 1401 TATAGTTGAGATCCAGATGATGAGTGAAGTGAAGGCTGATATTTTGAAGCACCAAGA 1460
Oy 529 pSerProLeuGluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrAr 549
Db 1461 CTCCCTTTAGAGCATCCGTCGTAGTCAGTACGTAATCTCGAGAGGTCACAG 1520
Oy 549 gLeuThrAspArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheI 569
Db 1521 GCTACACTGACCGCTGCTACTCATCTTCTGTCATCATGTCAGACTGTGACTTCTTAT 1580
Oy 569 eSerLysTyrSerAsnGlnLysAsnProHisCysValSerLeuTyrLysLysSerSerPr 589
Db 1581 AAGTAAGATATGTAACCAAGAAATCCACACTGTGTCCCTTTAACAAGATCAAGTCC 1640
Oy 589 oGluAspAspProThrCysLysThrLysGluPheThrAlaThrIleLeuAspSerAlaGl 609
Db 1641 TGAAGATGACCACTTCGCAACAAAGATTTTGGCCACACATTTTGCATTCAGCAGG 1700
Oy 609 yProLeuProAspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheTh 629
Db 1701 TCCTTCTCTGACTACTCTCTCCAGAAATTTCTTTTGAAGTACTACTGATTTAC 1760
Oy 629 rLeuTyrGlyMetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThVa 649
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Db 1761 ATTGTATGGATGCTTCAACAGCCCTCATGATCTACAGCCTGGAAAGAAATATCTACTGT 1820
Oy 649 lLeuPheIleTyrGlyGlyProGluValGlnLeuValAsnAsnArgPheLysGlyValLy 669
Db 1821 GCTGTTCTATATATGTTGCTCTCAGGTGCACTTGTGTATATATGCGTTTAAAGAGTCAA 1880
Oy 669 sTyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnAr 689
Db 1881 GTATTTCCGCTTGAATACCCCTAGCCCTCTAGTGTATGTTGTTAGTATGATGACACACAG 1940
Oy 689 gGlySerCysHisArgGlyLeuLysPheGluGlyAlaAlaPheLysTyrLysMetGlyGlnI 709
Db 1941 GGGATCCGTGTCAGCGAGGCTTAAATTTGAAGGCGCTTTAAATATATAAATG----- 1992
Oy 709 eGluIleAspAspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAs 729
Db 1992 ----- 1992
Oy 729 pLeuAspArgValGlyIleHisGlyTyrPheSerTyrGlyGlyTyrLeuSerLeuMetAlaLe 749
Db 1992 ----- 1992
Oy 749 uMetGlnArgSerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTyrPIL 769
Db 1993 -----GTTGCTATTGCTGGGCGCCAGTCACTCTGTGGAT 2027
Oy 769 ePheTyrAspThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnI 789
Db 2028 CTCTATATATACAGATACAGCAACGTTATATGCGTACCCCTGACAGATGAAAGAGG 2087
Oy 789 yTyrTyrLeuGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLe 809
Db 2088 CTATTACTTAGATCTGGCGCATGACAGCAAGAAAGTCCCTCAACCAAAATCCGTTT 2147
Oy 809 uLeuLeuLeuHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeu 829
Db 2148 ACTGCTCTTACATGATGTTCCGTGAGTGAAGATGTCATTTTGCATATCCACTATATTACT 2207
Oy 829 uSerPheLeuValAlaArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgH 849
Db 2256 CAGCATAGAGTTCCTGATGCGAGAACATTAAGACTGTCATCTTTGTCACCTTCA 2315
Oy 869 nGluAsnLeuGlySerArgIleAlaIleAlaLeuLysValIle 882
Db 2316 AGAAACCTTGATCAGCTATTGCTGCTTAAGTGATA 2355

RESULT 13
ABN59775
ID ABN59775 standard; cDNA; 2668 BP.
XX
AC ABN59775:
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 186.
XX
KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW antifertility; cerebroprotective; cyostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN WC020022660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001W0-US26015.
XX

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PR 11-SEP-2000: 200005-0659671.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX
 DR WPI: 2002-292408/33.
 DR P-PSDB: AB897362.
 XX
 PT An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis -
 XX
 PS Claim 1: SEQ ID NO 186; 509pp; English.
 XX
 CC The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
 CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a coding sequence of the
 CC invention.
 XX
 SO Sequence 2668 BP; 796 A; 564 C; 592 G; 716 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2668
 Score: 3771.00 Matches: 724
 Percent Similarity: 82.09% Conservative: 0
 Best Local Similarity: 82.09% Mismatches: 0
 Query Match: 80.23% Indels: 158
 DB: 24 Gaps: 2
 US-10-070-464-1 (1-882) x ABN59775 (1-2668)
 QY 1 MetAlaAlaIaIaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
 DB 234 ATGGCAGCAGCATGGAACAGACAGACAGCTGGGTGAGATATTGTAACCTGGCGACTGT 293
 QY 21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyValGluArgTyr 40
 DB 294 GAGGAGATATTGATCATCAGCATCGGCTAAATTTGAGAGCTTTTATGTGACGGGTAT 353
 QY 41 SerTrpSerIleuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
 DB 354 TCCTGGAGTCAGCTTAAAGCTGCTGCCGATACACGAAATATATCATGCTACATGATG 413
 QY 61 AlaLysAlaProHisAspPheMetPheValLysArgGlnAspProAspGlyProHisSer 80
 DB 414 GCTAAGCAGCAGCATGATGATTTTATGTTGTAAGAGAAATATCCAGATGAGACTCATTTCA 473
 QY 81 AspArgIleTyrTyrLeuAlaMetSerGlyLysAsnArgLysAsnThrLeuPheTyrSer 100
 DB 474 GACAGATATTATACCTGGCATGTCTGGTGGAGACAGAAATATACACTGTTTATTCT 533
 QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTyrLysProLeuLeu 120
 DB 534 GAATATCCCAAACTATCATATAGAGCAGCAGCTTATGCTCTTGGAGCCCTTTTG 593
 QY 121 AspLeuPheGlnIleThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuArg 140
 DB 594 GATCTTTTTCAG----- 605
 QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
 DB 605 ----- 605
 QY 161 ThrPheLeuPheGlnIleArgLysSerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180

DB 605 ----- 605
 QY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
 DB 606 -----CAACAACCTTTTAAGCCCAATCTAGTGAATCTAGTTGTCACACATACGATG 659
 QY 201 AspProLysLeuCysProAlaAspProAspTyrIleAlaPheIleHisSerAsnAspIle 220
 DB 660 GATCCAAATTTATGCTCCCTGCTGATCCAGACTGATTCCTTTTATACATACACAGATATT 719
 QY 221 TrpIleSerAsnIleValThrArgGluGluArgLeuThrTyrValHisAsnGluLeu 240
 DB 720 TGGATATCTAACAATCTATACACAGAGAAAGAGACTCTTATGTGCAAAATGACCTA 779
 QY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGlu 260
 DB 780 GCCAATGTGAGAGAGATGCGACATGAGTGGACTCCCTACCTTGTCTCCAGAAAGAA 839
 QY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
 DB 840 TTTGATAGATATTCTGGCTATTGGTGTGCCAAAGCTGAAACACTCCAGTGGTGT 899
 QY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
 DB 900 AAATCTTGAATTTCTATATGAGAAATGATCAACTGAGTGAATTTATTCATGTT 959
 QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
 DB 960 ACATCCCTATGTTGGAAACAGAGGAGATTCCTGCTTAATCTAAACAGGTACA 1019
 QY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
 DB 1020 GCAATCTTAAGTCACTTTTAAGATGTCAAGAAATATGATGATGCTCGAAGAGATC 1079
 QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 DB 1080 ATAGATCTCATAGATTAAGAACTAATTCACCTTTTGAATTTGAAAGAGATTGAA 1139
 QY 361 TyrIleAlaArgAlaGlyTyrPheProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
 DB 1140 TATATTCACAGAGCTGATGAGCTCTGAGGAGAAATATGCTGTCCATCTACTAGAT 1199
 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
 DB 1200 CGCTCCAGACTGCCCTACAGATAGTCTGATCTCACCTGAATATTATCCAGTGA 1259
 QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
 DB 1260 GATGATGTTATGAAAGCAGAGACTCATTCAGTCACTGCTGATTCGTGACGCCACTA 1319
 QY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
 DB 1320 ATTATCTATGAAGAAACAGACATCTGATTAATTCATGACATCTTTCATGTTT 1379
 QY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
 DB 1380 CCCCAAGTCAAGAGAGAAATGATTTATTTTCCCTGATGATCCAAACAGGTTTC 1439
 QY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
 DB 1440 CGTCATTTATACAAATTTATCATCTATTTTAAAGGAAACAAATTTAAACATCCAGTGT 1499
 QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
 DB 1500 GGGCTGCTCCCTCCAACTGATTTCAAGTGTCTATCAAAAGAGAGATGAATTTACAGT 1559
 QY 501 GlyIleTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
 DB 1560 GGTGAATGGGAGATTTCTGGCCGCGCATGATCTAATATCCAAAGTGAAGTCAAGCAGAG 1619
 QY 521 LeuValTyrPheGluGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
 DB 1620 CTGCTATATTTTGAAGCAGCAGCAAAAGACTCCCTTTAGAGCATCACCTGATGATCAGT 1679

QY 21 GluGluAsnIleGluSerGlnAspArgProLyLeuGluProPheTyrValGluArgTyr 40
 |||||
 Db 274 GAGGAGAAATATTGAATACAGCATCGCCAAATTTGAGACCTTTTATGTTGAGCGGTAT 333
 QY 41 SerTrpSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
 |||||
 Db 334 TCTGGAGTCAGCTTAAAGCTGCTGCCGATACAGAAATATCATGTGCTCATGATG 393
 QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
 |||||
 Db 394 GCTAAGGACACCATGATTTTCATGTTTGTCAAGAGATATCATCAGATGACCTCATTTCA 453
 QY 81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
 |||||
 Db 454 GACAGATCATATTACCTGCTGCTGCTGAGACAGAAATATCATGCTTTTATTTCT 513
 QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
 |||||
 Db 514 GAATTCCTCCAAACTATCATATAGAGCAGCTTAAATGCTCTCTTGGAAAGCCTCTTTTG 573
 QY 121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
 |||||
 Db 574 GATCTTTTTCAGGCAACACTGACGACTATGCAATGATTTCTGAGAGAGACTATTTAGA 633
 QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
 |||||
 Db 634 GAAAGAAACGCAATTCGACAGCTCGGAATTCCTTACATATTATCCACAGAGAGTGA 693
 QY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
 |||||
 Db 694 ACATTTCTGTTTCAGCCGCTAGTGAATTTATCACCTAAAGATGAGGGCCACAGAGA 753
 QY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
 |||||
 Db 754 TTATGCGCAACACCTTTAAGGCCCATCTAGTGGAAACTGTTGCTCCAAACATACGGATG 813
 QY 201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
 |||||
 Db 814 GATCCAAATTTATGCTGCTGCTGATCCAGACTGATGCTTTTATACATACCAACGATATT 873
 QY 221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
 |||||
 Db 874 TGGATATCTTACATCGTAAACAGAGAAAGAGAGACTCATTAATGCGCAATGAGCTA 933
 QY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
 |||||
 Db 934 GCCAATCATGGAAGATGCGCATATCAGCTGAGTGGCTTCTTGTCCCAAGAAAGAA 993
 QY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
 |||||
 Db 994 TTTGATAGATATTCTGCTATTGCTGCTGCCAAAGCTGAACACTCCACGTGGTGGT 1053
 QY 281 LysIleLeuAlaArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
 |||||
 Db 1054 AAATCTTATGATTTCTATATGAGAAATGAGAAATCTGAGGTGGAATATTCATGTTT 1113
 QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
 |||||
 Db 1114 ACATCCCTCATGTGTGGAACAACAGAGCAGATTCATTCCTGTTATCTTAACACAGGTACA 1173
 QY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
 |||||
 Db 1174 GCAAATCCTTAAAGTCACTTTTAAAGATGAGAAATATGATGCTGTAAGAGAGATC- 1232
 QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 |||||
 Db 1232 ----- 1232
 QY 361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
 |||||
 Db 1232 ----- 1232
 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400

Db 1232 ----- 1232
 QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
 |||||
 Db 1232 ----- 1232
 QY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
 |||||
 Db 1232 ----- 1232
 QY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysTrpGlyPhe 460
 |||||
 Db 1232 ----- 1232
 QY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
 |||||
 Db 1232 ----- 1232
 QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
 |||||
 Db 1232 ----- 1232
 QY 501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
 |||||
 Db 1233 -----CAAGTGATGAAGTCAGAGG 1253
 QY 521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisIleuTyrValValSer 540
 |||||
 Db 1254 CTGGTATATTATTTAAGGACACCAAGATCCCTTTTAAAGCATCACCTGTAGTACGTAGT 1313
 QY 541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
 |||||
 Db 1314 TACGTAATCTCTGAGAGGTGACAGAGCTGACTGACCGTGGCTATCTACTTTCTGCTGC 1373
 QY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
 |||||
 Db 1374 ATCAGTCAGCAGCTGTGACTCTTTATAGTAAAGTATAGTAACCAAGAAATCCACACTGT 1433
 QY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
 |||||
 Db 1434 GTGTCCCTTTTACAAAGCTATCAAGTCCGAGAGATGACCACTTGCAAAACAAAGAAATTTT 1493
 QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTrpThrProProGluIlePhe 620
 |||||
 Db 1494 TGGGCCACCACTTTTGCATTTCAGCAGGTCCTCTCTGACATATCTCTCCAGAAATTTTC 1553
 QY 621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
 |||||
 Db 1554 TCTTTGAAAGTACTACTGATTTTACATTGTATGGGATGCTTACAAAGCCTCATGATCTA 1613
 QY 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGly--ProGlnValGlnL 660
 |||||
 Db 1614 CAGCTTGGAAGAAATATCTTACTGTGCTGTTCATATATGCTGTCTCCACAGGTGAGT 1673
 QY 660 euValAsnAsnArgPheLysGlyValLysTyrPheArgGluAsnThrLeuAlaSerLeuG 680
 |||||
 Db 1674 TGGTGAAATATCGGTTTAAAGAGTCAAGATATTTCCGCTTGAAATACCTTACCTCTCTAG 1733
 QY 680 LysTyrValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluG 700
 |||||
 Db 1734 GTTATGTGGTTGTAGTATGATGACACAGGGGATCTGTCAACGAGGCTTAAATTTGAG 1793
 QY 700 LysAlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnT 720
 |||||
 Db 1794 CGCCCTTTTAAATATAAATATGCTCAATATGAAATTCAGCTGATGGAAGGACTCCAAAT 1853
 QY 720 TyrLeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTyrSerT 740
 |||||
 Db 1854 ATCTACGCTTCTGCATATGATTTTCACTTACATGCTGTGGGCAATCCAGCGTGTGCTCT 1913
 |||||
 QY 740 YrsGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaI 760
 |||||

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

QY 395 LeupheileProvalGlusaspvalMetGlvarGlnargLeuIleGluserValPro 414

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|||||
Db 601 TTATTAATCCAGTAGAAGATGATGTTATGGAAGGAGAGACTCATTCAGTACGCTT 660
QY 415 AspSerValThrProLeuIleIleTyrGluGluThrThrsplLeuIleHis 434
Db 661 GATTCTGTGAGCGCAATTAATATATGAAGAAACAACACATCTGGATTAATATCCAT 720
QY 435 AspIlePheHisValPheProGlnSerHisGluGluIleGluPheIlePheIleSer 454
Db 721 GACATCTTTCATGATTTTCCCAAGTACAGAGAGAAATTCAGTTATTTTGGCTCT 780
QY 455 GluCysLeuThrClyPheArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLys 474
Db 781 GAATGCAAAACAGGTTCCGTCATTATACAAATTAACATCTATTAAAGAAAGCAAA 840
QY 475 TyrLeuArgSerSerClyLeuProAlaProSerAspPheLysCysProIleLysGlu 494
Db 841 TATTAAGCATCCAGTGTGGCTGCTGCTCCAAAGTGAATTCAGTGTCTTATCCAAAG 900
QY 495 GluIleAlaIleThrSerClyGluTyrPgluValIleuGlyArgHisGlySerAsnIleGln 514
Db 901 GAGATGACATTAATCCAGTGTGAATGGAAAGTCTTGCGCGGATGGATATATCCAA 960
QY 515 ValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeuGluHis 534
Db 961 GTTGATGAAGTCAAGAGCGTGTATATTTGAAGGACCAACAACTCCCTTTAGAGCAT 1020
QY 535 HisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAspArgGly 554
Db 1021 CACCTTACCTAGTACGTTACGTAATCTCGAGAGGTGCAAGGCTGAGTACCGTAGC 1080
QY 555 TyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyrSerAsn 574
Db 1081 TACTCAGATCTTGTGTCAGTACAGTACAGCTGTGACTTTTATAGTAGTAGTAGAAC 1140
QY 575 GlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGlnAspProThr 594
Db 1141 CAGAAATCCACACTGTGTGCTCCCTTTACAACTATCAAGTCTGAAGATGACCAACT 1200
QY 595 CysLeuThrLysGluPheThrAlaThrIleLeuAspSerIleGlyProLeuProAspTyr 614
Db 1201 TGCAAACCAAGGAATTTTGGGCGCACATTTTGGATTCCACAGGTCCTCTCTGACTAT 1260
QY 615 ThrProGlnIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeu 634
Db 1261 ACTCCTCCAGAAATTTTCTCTTTTGAAGTACTAGTATTCATTGTATGGAGTCTC 1320
QY 635 TyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIleTyrGly 654
Db 1321 TACAACTCATGATGATCTACAGCTGGAAGAAATATCTACTGCTGTCATATATGCT 1380
QY 655 GlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsn 674
Db 1381 GGTCTCAGAGTGCAGTGTGTAATCGGTTTAAAGAGGTCAAGTATTTCCCGTTGAAT 1440
QY 675 ThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgLysSerCysHisArg 694
Db 1441 ACCCTAGCTCTCTAGGTTATGTGTGTAGTAGACAAACAGGGGATCCTTCACCGA 1500
QY 695 GlyLeuLysPheGluGluValAlaPheLysTyrLysMetClyGlnIleGluIleAspAspGln 714
Db 1501 GGCTTAAATTTGAAAGCGCTTAAATATAAATG----- 1536
QY 715 ValIleGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArgValGly 734
Db 1536 ----- 1536
QY 735 IleHisGlyTyrSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAsp 754
Db 1536 ----- 1536
QY 755 IlePheArgValAlaIleAlaGlyAlaProValThrLeuTyrPhePheTyrAspThrGly 774
|||||

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Db 1537 -----GTTCSTATTGCTGGGCCCCAGTCACTCTGTGATCTTCTATGATACAGCA 1587
QY 775 TyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySer 794
Db 1588 TACACGGAACTTATATAGGGTCACTCCGACCAAGAAATGAAGGCTATATTAAGGATCT 1647
QY 795 ValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeuHisGly 814
Db 1648 GTGGCCATGCAACAGAAAGTTCCCTCGAACCAAAATGTTTACTGCTTACATGCT 1707
QY 815 PheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeuValArg 834
Db 1708 TTCTGGATGAGATGTCATTTTGGCACATACAGATATATTAAGTGTAGAGC 1767
QY 835 AlieGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArgValPro 854
Db 1768 GGTGGAAGCCATATGATTAAGATCTATCTCAGGACAGACACACATTAAGAGTTCT 1827
QY 855 GluSerClyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySer 874
Db 1828 GAATCGGAGACATTAATGAACATGCACTTTTGCACATCCTTCACAGAAACCTTGATCA 1887
QY 875 ArgIleAlaIleLeuLysValIle 882
Db 1888 CGTATGCTGCTCTAAAGTGATA 1911

RESULT 16
ABK83323
ID ABK83323 standard; cDNA; 2617 BP.
XX
AC ABK83323;
XX
DE 12-AUG-2002 (first entry)
XX
CDNA encoding human DPPIV related serine protease DPP-2.
XX
Human: serine protease; dipeptidyl peptidase IV-related protein; DPPP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyslexia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001: 2001WO-US31874.
XX
PR 12-OCT-2000: 2000US-240117P.
XX
PA (FERR ) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
XX
PT P-PSDB; ABG61592.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
XX
PS Claim 1: Page 56-57; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly

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[illegible]

XX Qi S, Akinsanya KO, Riviere PJ, Junten J;
 PI WPI: 2002-444178/47.
 DR P-PSDB: ABG61604.
 XX
 PI New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT -
 PS
 PS Disclosure: Page 84-85; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related
 CC proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyslexias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABR63322-ABR63343 encode human DPPR proteins.
 XX
 SO Sequence 4219 BP; 908 A; 1320 C; 1190 G; 801 T; 0 other;

Alignment Scores:

Pred. No.:	8.4e-283	Length:	4219
Score:	2870.00	Matches:	517
Percent Similarity:	77.50%	Conservative:	134
Best Local Similarity:	61.55%	Mismatches:	187
Query Match:	61.06%	Indels:	2
DB:	24	Gaps:	2

US-10-070-464-1 (1-882) x ABK83335 (1-4219)

Qy	35	PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys	54
		: : : :	
Db	436	TTTCCAGGTGCGAAGACACTCTGTGGACGGGCTCCGGAGCATATCCACGGCAGCCGAC	495
Qy	55	TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp	74
		: : : :	
Db	496	TACTCGGGCTCATTTGTCAACAAGGGCCGCCACAGCATTCAGGTTTGTGCAAGACAGGAT	555
Qy	75	ProAspGlyProHisSerAspArgLLeTyrTyrLeuAlaMetSerGlyGluAsnArgLys	94
		: : : :	
Db	556	GAGTCTGGCCCCCATCTCCACCGGCTCTACTACCTGGGAACCATATGACCGGACAG	615
Qy	95	AsnThrLeuPheTyrSerGlnLeuProLysThrLLeAsnArgAlaValLeuMetLeu	114
		: : : :	
Db	616	AACCTCCCTCTACTCTGAGATATCCACAAGAGTCCGGAAAGAGGCTCTGCTCTCTG	675
Qy	115	SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg	134
		: : : :	
Db	676	TCTCTGGAAGCAGATGTCTGTGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG	735
Qy	135	GluGluGluLeuLeuArgGluArgLysArgLLeGlyThrValGlyLLeaLysSerTyrAsp	154
		: : : :	
Db	736	GAGGAGGAGCTGTGAGGAGGACGGAAACGCCCTGGGGGGCTTCGGGCATCACCTCTACGAC	795
Qy	155	TyrHisGlnGlySerGlyThrPheLeuPheMetLacGlySerGlyLLeTyrHisValLys	174
		: : : :	
Db	796	TTTCCACACCGAGAGTGGCTCTCTCTTCCAGGCCACGACAACACCTCTTCCACTGGCCG	855
Qy	175	AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer	194
		: : : :	
Db	856	GACGGCGGCAAGAACGGCTTATGTGTGTCCCTTATGAAACCGCTGGGAATATCMAGACCCAG	915
Qy	195	CysProAsnLLeaArgMetAspProLysLeuGlySerProLLeaAspProAspTrpLLeaLaph	214

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Db      916  TCGTCAGGGCCCGGATGACGCCAAATCGCCCTGCAGACCTGCTCTCTCTC
Oy      215  ILeHisSerAsnAspIleThrPheLeuValThrArgLeuValArgLeuThr
Db      976  ATCAATPACAGCGCTGGGTGGCCAACTGAGACAGCGAGAGCGCGGCTGACC
Oy      235  TyrValHisAsnGluLeuAlaAsnMetGluLeuAspAlaArgSerAlaGluAlaThr
Db      1036  TTCCTGCACCAAGCTTATCCATGTCCTGATGACCCCAAGTCGTGGGTGGCCACC
Oy      255  PheValLeuGluGluLeuPheAspArgTyrSerGlyTyrTrpTyrProLysAlaGlu
Db      1096  TTCGTATACAGAGAGATTGACCCCTTCACGTGGTACTGGTGGTGGCCACAGCTCC
Oy      275  ThrThrProSerGlyGly---LysIleLeuArgIleLeuThrGluAsnAspGluSer
Db      1156  TGGGAAGTTCCAGAGGCTCCAGACGCTCGAATCTGTATGAGAAAGTCATGAGTCC
Oy      294  GluValGluIleIleHisValThrSerProMetLeuGluThrArgAlaAspSerPhe
Db      1216  GAGGTGGAGTCACTACGTCCTCTCCCTGCGCTAGAAAGAAAGAGAGACTCGTAT
Oy      314  ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet
Db      1276  CGGTACCCAGAGAGAGAGCAAGAAATCCCAAGATTGCTTGAACGTGGCTGATTCAG
Oy      334  IleAspAlaGluGluValArgIleIleAspValIleAspLysGluLeuIleGluProPheGlu
Db      1336  ACCGACAGCGAGGCAAGATCGTCTGACCCAGAGAGAGAGAGAGTGGTGGCCCTTCAGC
Oy      354  IleLeuPheGluGluValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyTyr
Db      1396  TCCCTCTTCCCGAAGGTGGAGTACATGCGCAGCGCGGTGAGCAGCCGCGCAATAC
Oy      374  AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGluIleValIleSerPro
Db      1456  GCGTGGGCAATGTCCTGAGACGGCCCGACAGTGGCTCCAGCTCGCTCCGCCCGC
Oy      394  GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal
Db      1516  GCCCTGTTCATCCGAGCAGACAGAGATGAGAGACAGCGCTACCTCGCAAGCTGTC
Oy      414  ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleThrIleAsnIle
Db      1576  CCAGAGAATGTCAGCGCTGTGTGTGTACGAGAGAGTCCCAACGCTGTGATCAATGTT
Oy      434  HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe
Db      1636  CATGACATCTCTATCCCTTCCCTCCCAATCAGAGAGAGAGAGAGAGCTTCTTCCTCCG
Oy      453  AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu
Db      1696  GCCAATGATGCAAGACCGGCTCTGCATTTGTACAAATCCACCGCGCTTAAATCC
Oy      473  SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle
Db      1756  CAGGCGCTGATGGAGTGGAGCCCTTCAGCCCGGGAAGATTAATTAAGTCCCATTT
Oy      493  LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGluArgHisGlySerAsn
Db      1816  AAGGAGAGATTCCTGTGACAGCGGAGATGGAGATTGGCGAGGCGAGCTCCACAG
Oy      513  IleGluValAspGluValArgArgLeuValTyrPheGluGluIleThrLysAspSerProLeu
Db      1876  ATCTGGGTCAATGAGAGACCAAGCTGTGTACTTCAGAGGCAACCAAGAGACGCGCTG
Oy      533  GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp
Db      1936  GAGCACACCTCTACCTGTGACGTATGAGCGCGCGAGATCGATCGCTCACACAG
Oy      553  ArgGlyTyrSerHisSerCysLysIleSerGlnHisCysAspPheIleSerLysTyr

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Db      1996  CCCGCTTCCATAGCTGCTCCATGAGACAGAACTTGCAATGTTGTCACCACTAC
Oy      573  SerAsnGluLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp
Db      2056  AGCAGGTGAGACAGCGCGCTGTCGACGTCTACAAAGTGTAGCGCGCCGAGCAGCAGC
Oy      593  ProThrCysLysThrLysGluPheThrAlaThrIleLeuAspSerAlaGlyProLeuPro
Db      2116  CCCCTGCACAGAGCGCGCTTCTGGGCTGACATGATGGAGGACAGCAGCTCCCGCCG
Oy      613  AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly
Db      2176  GATTATGTTCTCCAGATCTTCATTCACACCGCGGTGATGGCGGCTTCTACGGC
Oy      633  MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle
Db      2236  ATGATCTACAGGCCCCACAGCTTTCAGCCAGGAGAGAGACACCCACCTGCTTTGTA
Oy      653  TyrGlyGlyProGluValGluLeuValAsnAsnArgPheLysGluValLysTyrPheArg
Db      2296  TATGAGAGCGCCCGAGGTGAGTGTGAATTACTCTTCAAGGATCAAGTACTGGCG
Oy      673  LeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgGlySerCys
Db      2356  CTCACACACTGGCTCCCTGGGCTACCGCGCTGTGTGTGTTTACGCGAGGGGCTCTG
Oy      693  HisArgGlyLeuLysPheGluGluValAlaPheLysTyrLysMetGlyGlnIleGluLeuAsp
Db      2416  CAGCAGGCTTCCGTTCTGAGAGGCGCTCAGAAACCAAAATGGCCAGGTGAGATCGAG
Oy      713  AspGluValGluGluLeuGluGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg
Db      2476  GACACAGGTGAGGCGCTGCTGCGCCGAGAAATATGCTTCATCAGCAGCAGCAGCA
Oy      733  ValGlyIleHisGlyThrPheSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg
Db      2536  GTTGCATCATGCTGCTGCTACGGGGCTCTCTCTGCTCATGGGCTTAATTCACAGC
Oy      753  SerAspIlePheArgValAlaIleAlaGluAlaProValThrLeuThrPheThrAsp
Db      2596  CCCAGGTGTTCAAGGTGGCGCATCGCGGCGCCGCTGACCGTGTGATGGCTTACGAC
Oy      773  ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrLeu
Db      2656  ACAGGCTACACTGACGCTACATGAGAGCTCCCTGAGAACACACGACGCTGTAGAGCG
Oy      793  GlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeu
Db      2716  GGTTCGCTGGCTGACAGCTGGAGAGCTGCCCAATGAGGCCACCGCTTGTATCTTC
Oy      813  HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu
Db      2776  CACGGCTTCTGAGCAAAACGTCGACTTTTCCACAAACGTTCTCGTCCCAACTG
Oy      833  ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGluGlnArgHisSerIleArg
Db      2836  ATCCGAGAGGAGAACTTACACGACTCCAGATCCCAACAGAGAGACACATATTCCG
Oy      853  ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu
Db      2896  TGGCCGAGTGGGCGAGCACTATGAAAGTACGTTGCTGACATCTTCTACAGAAATACCTC

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RESULT 18
 ABR83333
 ID ABR83333 standard; cDNA: 4302 BP.
 AC ABR83333;
 XX 12-AUG-2002 (first entry)
 XX DT
 XX CDNA encoding human DPRP-2 splice variant #1.
 DE Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW

QY	473	SerLYSTyrLysAspSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle	492
Db	1756	CAGGGCTACAGTTCGACTGAGCCCTTCAGCCCGGGGGAAGATGAATTTAAGTCCCAATT	1815
QY	493	LysGLuGLuIleAlaIleThrSerGlyGlyTyrGluValLeuGLyArgHisIleSerAsn	512
Db	1816	AAGAAAGAGATTCGCTCGACCAAGCGGGAATGGAGGTTTGGCGGACCGCTCCACAG	1879
QY	513	IleGlnValAspGlyValArgAspLeuValTyrPheGluGlyThrLysAspSerProIleu	532
Db	1876	ATTCGGGTCATGAGAGACCAACCTGGTACTTCCAGGGCACCAAGACAGCCGCTG	1935
QY	533	GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgIleuThrAsp	552
Db	1936	GAGCACCAACCTCTACGTGCTGACACTGAGAGCGCGCGAGATCGTACGCTCCACAG	1999
QY	553	ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPheIleLeuLysTyr	572
Db	1996	CCCGACTTCCTCCATCTCTCTCCATAGCCAAACCTTCGACATGTCCTCAGCCACATAC	2055
QY	573	SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProLysAsp	592
Db	2056	AGCAGCGTACAGCACCGCGCCCTCGTGCAGCTGTACAACTGAGCGCGCCGACAGCAC	2115
QY	593	ProThrCysLysThrLysGluPheThrPalaThrIleLeuAspSerAlaGlyProLeuPro	612
Db	2116	CCCCGACACAAGCACGCCCTCTCTGGCGTACGATGATGAGGACAGCCAGCTGCCCCCG	2179
QY	613	AspTyrThrProProGluIlePheSerPheGluSerThrThcGlyPheThrIleuTyrGly	632
Db	2216	GATTATGTCTCTCCAGAGATCTTCATTTCCACACCCGCTCGATGTCGGGCTCTACGCG	2235
QY	633	MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrTyrProThrValLeuIle	652
Db	2236	ATGATCTACAAAGCCCCCGCTCTGACGCCAGGGAAACACCCCGCTCTCTTTGTGA	2295
QY	653	TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg	672
Db	2296	TATGAGAGCCCCCAGGTGCGATGTGTGAATAACTCTTCAAAAGCATCAAGTACTTGGCG	2355
QY	673	LeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgLysCys	692
Db	2356	CTCACACACACTGGGCTCCGCGGCTACAGCCGTGGTGTATTGACGCGAGGGCTCTGT	2415
QY	693	HisTyrGlyLeuLysPheGlnGlyAlaPheLysTyrLysMetGlyIleIleIleIleIleIle	712
Db	2416	CAGCGAGGGCTTCGTTCCGAAGGGGCCCTGAAAAACCAATGGGCCAGGTGGAGATCGAG	2475
QY	713	AspGlnValGlnGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg	732
Db	2476	GACCAGGTGAGGGCTGCGATTCGTGGGCCGAGAGATGGCTTCATGCACCTGAGCGGA	2535
QY	733	ValGlyIleHisGlyTyrPserTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg	752
Db	2536	GTTCCCATTCATGGCTGCTCTACAGGGGGCTTCCTCCCTCATGGCGTAATCCACAG	2595
QY	753	SerAspIlePheAspValAlaIleAlaGlyAlaProValThrLeuTyrPheIleTyrAsp	772
Db	2596	CCCCAGGTTCACAGGTGGCCATTCGCGGGTCCCGCCGCTCACCTCTGATGGCTACGAC	2655
QY	773	ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnLysTyrTyrLeu	792
Db	2656	ACAGAGGTACACTGAGCCCTCATGTGAGACGTCCGGAACACACAGACGCTATAGAGCG	2715
QY	793	GlySerValAlaMetGlnAlaGlyLysPheProSerGluProAsnArgLeuLeuLeuLeu	812
Db	2716	GGTTCCTCGGGCCCTGCACGTGGGAAAGCTGCCCAATGAGCCCAACCGCTTGTATCTTC	2779
QY	813	HisGlyPheLeuAspGlnAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu	832
Db	2776	CAGCGCTTCCTCGAGCAAAACGTGCACTTTTCCACACAAACTCTCTGCTCCCAACTG	2833
QY	833	ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg	852

Dn	2836	ATCGACGACGGAAACTTACAGCTCCAGATGTACCACCCAGACAGACAGTAFTTCGC	2895
Oy	853	ValProGluSerGlytGIunHISITyTGtuleuNHSLenLeuNHISITyLengInGLuanLen	872
Dn	2896	TGCCCCAGTCGGCGCAGCACTATGAAGTCACGTTCTGCTCACCTTCTCATAGAGAATAATCCTC	2955
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RESULT 19			
ID	AAD38954	standard; cDNA; 3024 BP.	
XX			
AC	AAD38954;		
Dn	23-SEP-2002	(first entry)	
XX			
DE	Human dipeptidyl peptidase 9 (DPP9) cDNA.		
XX			
KW	Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;		
RW	autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;		
KM	graft rejection; antiabietic; antiinflammatory; immunosuppressive;		
KW	antiviral; enzyme; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..2910	
FT		/tag= a	
FT		/product= "human DPP9 protein"	
FT		/transl_except= (pos: 1120..1122, aa:Gln)	
FT		/note= "CDS does not include start codon"	
FT		/partial	
XX			
PN	WO200234900-A1.		
XX			
PD	02-MAY-2002.		
XX			
PF	29-OCT-2001; 2001MO-AU01388.		
XX			
PR	27-OCT-2000; 2000AU-0001078.		
XX			
PA	(UNSY) UNIV SYDNEY.		
XX			
PI	Abbott CA, Gorrell MD;		
XX			
DR	WPI: 2002-454646/48.		
XX			
DR	P-PSDB; AAE24168.		
XX			
PT	New dipeptidyl peptidase (DPP) peptides, useful for screening		
XX	Inhibitors of DPP catalytic activity, which may be employed to treat		
PT	e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft		
XX	rejection and HIV infection -		
PS	Example; Fig 4; 91pp; English.		
XX			
CC	The present invention relates to dipeptidyl peptidase (DPP) proteins and		
XX	polynucleotides encoding such proteins. The DPP peptides are useful for		
CC	screening inhibitors of DPP catalytic activity. The inhibitors are useful		
XX	for treating neoplasias, type II diabetes, cirrhosis, autoimmunity, graft		
CC	rejection and HIV (human immuno deficiency virus) infection. The present		
XX	sequence is human DPP9 cDNA.		
SQ	Sequence 3024 BP; 624 A; 973 C; 875 G; 552 T; 0 other:		
<hr/>			
Alignment Scores:			
Pred. No.:	2, 63e-282	Length:	3024
Score:	2863.00	Matches:	516
Percent Similarity:	77.38%	Conservative:	134
Best Local Similarity:	61.43%	Mismatches:	188
Query Match:	60.91%	Indels:	2
DB:	24	Gaps:	2

Db	1468	GGCCGTTTCATCCCGACACAGAAATGAGGACGCGCTAGCCTTCACAGAGCTGTC	1522
Qy	414	ProAspSerValThrProLeuAlaIleThrGlyClnIuThrThrAspIleThrPileAsnIle	433
Db	1528	CCGAGGAAATGTCACGCCCTATGTGGTACAGAGAGGTCCACCAAGCTTGATCAATGTT	158
Qy	434	HisAspIlePheHisValPheProGlnSerHis--GluGluGlnIleGluPheIlePhe	4522
Db	1588	CATGACATCTTCTTATACCTTCCCCCATACAGAGGACAGCAGACGCTCTTCTCC	164
Qy	453	AlaSerGlyCysLysThrGlyPheArgHisLeuThrLysIleSerIleLeuLysGlu	472
Db	1648	GCCATGATGAATGACAGACCGGCTTGCCATTGTACAAAGCATCCGCGTTTAAATCC	170
Qy	473	SerLysThrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysProIle	492
Db	1708	CAGGCTCAGATTGGAGTGAACCCCTTACGCCCGGGAAGATGAATTAAGTGCCTATT	176
Qy	493	LysGluGlnIleAlaIleThrSerGlyLysIleProGlnValLeuGluArgHisGlySerAsn	512
Db	1768	AAGGAAGATTTGGCTCTACCCACGCGGTAAATGGAGGTTTGGGAGAGCAGCGCTCCAG	182
Qy	513	IleGlnValAspGluValArgArgLeuValIleArgPheGluGlyThrLysAspSerProLeu	532
Db	1828	ATCTGGTGTCATAGAGACACCAAGCTGGTGTACTTCCAGGCGACCAAGACAGCGCTG	188
Qy	533	GluHisHisLeuThrValValSerThrValAsnProGlnGlyValIleArgLeuThrAsp	552
Db	1888	GAGCAACACCTCTACGTGTGTAGCATGACGGCGCGCGAGATCAACCGCTCACCCACG	194
Qy	553	ArgGlyThrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLys	572
Db	1948	CCGCGCTTCTCCATAGCTGCTCCATGAGGCCAGAACTTCCACATGTTCTGTACGCACTAC	200
Qy	573	SerAsnGlnLysAsnProHisLysCysValSerLeuThrLysLeuSerSerProGlnAsp	592
Db	2008	AGCAGCGTAGAGACGCCCGCTGCGTGCATCAACAAGCTGACGCGCGCCGACGAC	206
Qy	593	ProThrCysLysThrLysGluPheThrAlaThrIleLeuAspSerAlaGlyProLeuPro	612
Db	2068	CCCGTCGACACAGACGCCCGCTTGTGGCTGACATGATGAGGACGACACCTGCCCCG	212
Qy	613	AspThrThrProProGlnIlePheSerPheGluSerThrThrGlyPheThrLeuThrGly	632
Db	2128	GATTATGTTCTCCAGAAATCTTCCATTTCACACCGCGCTGGATGTCCGCTTACGGC	218
Qy	633	MetLeuThrLysProHisAspLeuGlnProGlnLysLysThrProThrValLeuPheIle	652
Db	2188	ATGATCTCAAGACCCCGACGCGCTTGACAGCAGGAAGACCCCGACGTCCTTTGTA	224
Qy	653	ThrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysThrPheArg	672
Db	2248	TATGAGAGCCCCCAAGCTGCACCTGTGTAACTCTTCAAAAGCAATCAAGTACTTCCG	230
Qy	673	LeuAsnThrLeuAlaSerLeuGlyThrValValValIleAspAsnArgGlySerCys	692
Db	2308	CTCAACACACTGGCTCCCTTGGGCTACGCGCTGGTGTGATTGACGGCAGGGGCTCTGT	236
Qy	693	HisArgGlyLeuLysPheGlnGlyAlaPheLysThrLysMetGlyGlnIleGlnIleAsp	712
Db	2368	CAGCGAGGCGTTGGTTGGAAGGGGGCCGTGAANAACCAATGGGCCAGTGGAGATCGAG	242
Qy	713	AspGlnValGluGlyLeuGlnThrLeuAlaSerArgThrAspPheIleAspLeuAspArg	732
Db	2428	GACCGAGGTGGAGGGCTGCACCTTGCGCCAGAAAGATGAGCTTCAATCGACCTGACCGA	248
Qy	733	ValGlyIleHisGlyTrpSerThrGlyGlyThrLeuSerLeuMetAlaLeuMetGlnArg	752
Db	2488	GTTGCCATTCATGGCTGGCTCTTACAGGGGGGCTCTCTCGCTCAAGGGGCGCTAAATCCACAG	254
Qy	753	SerAspIlePheArgValAlaIleAlaGlyValAlaProValThrLeuThrPileThrArg	772

Db 2348 CCCCAGGTGTTCAGTGGCCATCGCGGTGCCCCGCTACCGCTGTGATGGCCCTACGAC 2607
 Oy 773 ThGlyTyrThrGluArgTyrMetGlyHisProaspGlnasnGluGlnGlyTyrTyrLeu 792-
 Db 2608 ACAGGCTACACTGAGCCCTACATGAGCTCCCTGAGAACACACGACGCGCTATGAGCGC 2667
 Oy 793 GlySerValAlaMetGlnAlaGluLysPheProSerGluProaspArgLeuLeuLeu 812
 Db 2668 GGTTCCTGGCCCTGCACAGCGAGACAGCTGCCCAATGAGCCCAACCGCTTCTTATCCTC 2727
 Oy 813 HisGlyPheLeuaspGluasnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
 Db 2728 CACGCTCTCCGACGAAACGTCACCTTTTCCACACAACTTCCTGCTCCCAACTC 2787
 Oy 833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852
 Db 2788 ATCCGACAGAGGAACCTTACACAGCTCCAGATCTACCCCAACGAGACACAGATATTCGC 2847
 Oy 853 ValProGluSerGlyLysHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluasnLeu 872
 Db 2848 TGCCCCAGTGGCGGAGACACTATGAGTACAGTCTTACTGCACTTCTTACAGAAATACCTC 2907

RESULT 20

AAD38957 standard; DNA; 2495 BP.
 ID AAD38957

AC AAD38957;

DF 23-SEP-2002 (first entry)

XX Human dipeptidyl peptidase 4 (DPP4)-like 2 DNA.

KM Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
 KM autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
 KM graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
 KM antiviral; enzyme; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT CDS 1..2493

FT //tag- a
 FT /product- "Human DPP4-like 2 protein"
 FT /transl_except- (pos: 703..705, aa:Gln)
 FT /note- "CDS does not include start codon"
 FT /partial

XX MO200234900-A1.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001MO-AU01388.

XX 27-OCT-2000; 2000AU-0001078.

XX (UNSY) UNIV SYDNEX.

XX Abbot CA, Gorrell MD;

XX PI AAE24171.

XX DR P-PSDB; AAE24171.

XX PT New dipeptidyl peptidase (DPP) peptides, useful for screening

XX PT inhibitors of DPP catalytic activity, which may be employed to treat

XX PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft

XX PT rejection and HIV infection -

XX PS Disclosure; Page 86-88; 91pp; English.

XX CC The present invention relates to dipeptidyl peptidase (DPP) proteins and

XX CC polynucleotides encoding such proteins. The DPP peptides are useful for

XX CC screening inhibitors of DPP catalytic activity. The inhibitors are useful

CC rejection and HIV (human immuno deficiency virus) infection. The present
 CC sequence is human DPP4-like 2 DNA.
 XX SQ Sequence 2495 BP; 535 A; 783 C; 696 G; 481 T; 0 other;

Alignment Scores:

Pred. No.: 1,44e-279 Length: 2495
 Score: 2835.00 Matches: 512
 Percent Similarity: 77.47% Conservative: 131
 Best Local Similarity: 61.69% Mismatches: 185
 Query Match: 60.32% Indels: 2
 DB: 24 Gaps: 2

US-10-070-464-1 (1-882) x AAD38957 (1-2495)

Oy 45 LeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetAlaLysAlaPro 64
 Db 1 CTCCGAGCATCATCCACCGCAGCGGAGTACTCGGCTCATATGTCACCAAGCGCC 60
 Oy 65 HisAspPheMetPheValLysArgAsnAspProaspGlyProHisSerAspArgIleTyr 84
 Db 61 CACGACTTCCAGTTTGTGCGAACAACGAGATGAGTGGCCGCCCTCCACCGCTCTAC 120
 Oy 85 TyrLeuAlaMetSerGlyLysArgLysArgLysAnThrLeuPheTyrSerGluIleProLys 104
 Db 121 TACCTGGGAATGCCATATGCGAGCGGAGAACTCCCTCTACTCTGAGATTCCCAAG 180
 Oy 105 ThrIleAsnArgAlaAlaValLeuMetLeuSerTyrPheProLeuAspLeuPheGln 124
 Db 181 AAGTCCGGAAGAGAGCTGTGCTGCTCTGCTGAGAGAGAGATGATGATATTCAG 240
 Oy 125 AlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArgLysArg 144
 Db 241 GCCACGCGCCACCATGGGGTGTACTCTCGGAGAGAGAGTCTGAGAGAGCGGAACGC 300
 Oy 145 IleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGlyThrPheLeuPhe 164
 Db 301 CTGGGGCTTCTGGCATCACCCTCTACGACTCCACACGAGAGAGTGGCTTCTCTTC 360
 Oy 165 GlnAlaGlySerGlyIleTyrHisValLysAspGlyIleProGlnGlyPheThrGln 184
 Db 361 CAGCCACAGACAGCCCTCTCTCTCTCCGCGCGCGGCAAGACGCTTCATGCTGCC 420
 Oy 185 ProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMetAspProLysLeu 204
 Db 421 CGTATGAACCCGTCGAAATCAAGACCCAGCTCAGAGGCCCGGATGAGACCCCAATC 480
 Oy 205 CysProAlaAspProAspTyrPheAlaPheIleHisSerAsnAspIleTyrPheSerAsn 224
 Db 481 TGCCCTGCCGACCCTGCTCTCTCTCTCAACAATAACAGCAGCTGTGGTGGCCAAC 540
 Oy 225 IleValThrArgGluGluArgLysLeuThrTyrValHisAsnGluLeuAlaAsnMetGlu 244
 Db 541 ATCGAGACAGCGGAGCGGCGGCTGACCTTCCACCAAGCTTATATCAAGTCTCTCG 600
 Oy 245 GluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGluPheAspArgTyr 264
 Db 601 GATGACCCCAAGTCTGGGGGTGGTGGCCACCTCTCATACGAGAAGTTCGACCGCTC 660
 Oy 265 SerGlyTyrTrpTyrCysProLysAlaGluThrThrProSerGlyGly---LysIleLeu 283
 Db 661 ACTCGTACTGTGTGTCGCCACAGCCTCTCGGAAGTTCAGAGGCTTCACAAACGCTG 720
 Oy 284 ArgIleLeuTyrGluGluAsnAspLysGluValGluIleIleHisValThrSerPro 303
 Db 721 CGAATCTGTATGAGAGTGTGATGATGAGGTGAGATTCATGACGCTCTCTCT 780
 Oy 304 MetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThrAlaAsnPro 323
 Db 781 GCGCTAGAAGAAAGAGACGACTGTATCGATACCCAGAGAGGACAGAAATAATCC 840
 Oy 324 LysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIleIleAspVal 343

Db 841 AAGATTGCTTTGAACCTGCTGAGTTCACAGCTACAGCCAGGCGCAAGTCTCTGACC 900
 QY 344 ILASPLSGIleuIleGIInProPheGIILleuPheGIuValGIuTYrTLeuAla 363
 Db 901 CAGGAGAGAGGTGGTGGTCCCTTCAGCTGCTGTTCGCCAAGGGAGTACATCGCC 960
 QY 364 ATGAGAGIYrPThrProGIuGIuLYSTYrAlaTrpSerIleLeuLeuAspAspSerGI 383
 Db 961 AGGGCCGGGTGAGCCGGGATGGCAATACGCTGGGCCATGTTCCTGAGCCGCCCCAG 1020
 QY 384 ThrArgLeuGIuValLeuIleSerProGIuLeuPheIleProValGIuAspAspVal 403
 Db 1021 CAGTGGCTCAGGTCTGCTCTCCGCCGCCCTTTCATCCCGACACAGCAAGTAC 1080
 QY 404 MetGIuArgGIuIleGIuIleGIuSerValProAspSerValThrProGIuIleTYr 423
 Db 1081 GACAGCGGCTACCTCTGCGACAGCTGCTCCAGCAATGTCCAGCCGTATGGGTAC 1140
 QY 424 GluGIuThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPheProGIuSer 443
 Db 1141 GAGAGAGTCAACAAGCTGTGATCATGTATGATGACATCTTCATATCCCTCCGCCATCA 1200
 QY 444 His---GluGIuIleGIuPheIlePheAlaSerGIuCYSTYrThrGIuPheArgHis 462
 Db 1201 GAGGAGAGGAGAGCTTCCTCTCCGCCCAATGAATGAAGCAAGCCGCTTCGCAT 1260
 QY 463 LeuTYrLysIleThrSerIleLeuLysGIuSerLysTYrLysArgSerSerGIuLeu 482
 Db 1261 TTGTACAAATCAACCGCGCTTTTAAATCCAGGCGTACATTTGGATGGAGCCCTTCAGC 1320
 QY 483 ProAlaProSerAspPheLysCYSProlIleLysGIuIleAlaIleThrSerGIuLeu 502
 Db 1321 CCGGAGAAATGAATTAATGATCCCATTAAGAGAGATGGTGTGACACGGGTGAA 1380
 QY 503 TrpGIuValLeuGIuArgHisGIuSerAsnIleGIuValAspGIuValArgGIuVal 522
 Db 1381 TGGAGGTGTTTGGCGAGCGCGCTCCAAAGATGGGTGATGAAGACCAAGCTGCTG 1440
 QY 523 TyrPheGIuGIuTYrLysAspSerProLeuGIuHisIleLeuTYrValIleSerTYrVal 542
 Db 1441 TACTTCAGGGCAACAAGACAGCCGCTGAGACACCACTTACGTGGTCAAGTATGAG 1500
 QY 543 AsnProGIuGIuValThrArgLeuThrAspArgGIuTYrSerHisSerCYSTYrSer 562
 Db 1501 GCGGCGGCGAGATCGATCGCTCACACAGCGCGCTTCCTCATACCTGCTCCATGAGC 1560
 QY 563 GluHisCYSPhePheIleSerLysTYrSerAsnGIuLysAsnProHisCYSTYrSer 582
 Db 1561 CAGAACTTCGACATGTTCGACCACTACAGAGCGTGAGCAACGCCCTGCGTGCAC 1620
 QY 583 LeuTYrLysLeuSerSerProGIuAspAspProThrCYSTYrThrLysGIuPheTrpAla 602
 Db 1621 GTCTACAGGTGAGCGGCCCGACAGACAGCCCTGCACAAAGCAAGCCCTCTGGGCT 1680
 QY 603 ThrIleLeuAspSerAlaGIuProLeuProAspTYrThrProGIuIlePheSerPhe 622
 Db 1681 AGCATATGAGAGCAGCAGCAGCTGCCCGGATATATGTCTCCAGAGATCTTCATTTTC 1740
 QY 623 GluSerThrThrGIuPheThrLeuTYrGIuLysLeuTYrLysProHisAspLeuGIuPro 642
 Db 1741 CACAGCGGCTGAGTGTGCGCTTACGGGATATCTTCAAGGCCCGCGCTTGCACCCA 1800
 QY 643 GlyLysLysTYrProThrValLeuPheIleTYrGIuLysProGIuValGIuLeuValAsn 662
 Db 1801 GGGAGAGAGACCCCGCTCTTTGTATATGAGAGCCCGCAGGTGCAAGCTGTGAAT 1860
 QY 663 AsnArgPheLysGIuValLysTYrPheArgLeuAsnThrLeuAlaSerLeuGIuTYrVal 682
 Db 1861 AACTCTTCAAGAGCATCAAGTACTGCGGCTCAACACACTGGGCTCTCGGGCTACGCC 1920
 QY 683 ValValValIleAspAsnArgLysSerCYSHisArgGIuLeuLysPheGIuAlaPhe 702
 Db 1921 GTGGTGTGATTGACGCGAGGCTCTGTTCACGAGGAGGCTTGGTTGCAAGGGGCCCTG 1980

QY 703 LysTYrLysMetGIuGIuIleGIuIleAspAspGIuValGIuGIuLeuGIuTYrLeuAla 722
 Db 1981 AAAAACCMAATGGGCCAGGTGGAGATGAGAGACCAGGTGAGAGGCTGCAAGTTCGTGGCC 2040
 QY 723 SerArgTYrAspPheIleAspLeuAspArgValGIuIleHisGIuTYrSerTYrGIuGIu 742
 Db 2041 GAGAAATGATGGCTTCATGCACTGAGCGAGATTGGCATATGGCTGTGCTCAAGGGGCG 2100
 QY 743 TyrLeuSerLeuMetAlaLeuMetGIuArgSerAspIlePheArgValAlaIleAlaGIu 762
 Db 2101 TTCCTCTCCCTCATGGGGCTTAATCCACAGCCCGAGGTGTTCAGAGGTGGCATTCGGCGCT 2160
 QY 763 AlaProValThrLeuTYrPheTYrAspThrGIuTYrThrGIuArgTYrMetGIuHis 782
 Db 2161 GCCCGGTCACCGCTGTGATGGCTTACGACACAGGTACATGACGCTTACATGGAGCTC 2220
 QY 783 ProAspGIuAsnGIuGIuTYrTYrLeuGIuLysSerValAlaMetGIuAlaGIuLysPhe 802
 Db 2221 CTTGAGAAACAACGACGCGCTATGAGCGGCTTCCTGGCCCTGACGAGTGGAGAACTG 2280
 QY 803 ProSerGIuProAsnArgLeuLeuLeuHisGIuLysPheLeuAspGIuAsnValHisPhe 822
 Db 2281 CCCAATGAGCCCAACCCCTTCTTATCTCCACGGCTTCTCTGGACGAAACGTCCACTTT 2340
 QY 823 AlanHisThrSerIleLeuLeuSerPheLeuValArgAlaGIuLysProTYrAspLeuGIu 842
 Db 2341 TTCCACACAAACTCTCTGCTCCCAACTGATCCGACAGAGGAACCTTACAGCTTCAG 2400
 QY 843 IleTYrProGIuGIuArgHisSerIleArgValProGIuSerGIuGIuIleTYrGIuLeu 862
 Db 2401 ATCTACCCCAACGAGACACAGATATTCGCTGCCCGGAGTCCGGGCGAGCACTATGAAGTC 2460
 QY 863 HisLeuLeuHisTYrLeuGIuGIuAsnLeu 872
 Db 2461 ACCTTACTGCATTTCTTACAGAAATACCTC 2490
 RESULT 21
 AAD38955
 ID AAD38955 standard; cDNA: 3287 BP.
 AC AAD38955;
 DT 23-SEP-2002 (first entry)
 XX
 DE Alternative version of murine dipeptidyl peptidase 9 (DPP9) cDNA.
 XX
 KW Murine; dipeptidyl peptidase; DPP; neoplasia; cirrhosis; HIV infection;
 KW human immune deficiency virus; graft rejection; cytostatic; autoimmunity;
 KW type II diabetes; antidiabetic; antiinflammatory; immunosuppressive;
 KW antiviral; enzyme; gene; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FH CDS 1..2610
 FT /tag= a
 FT /product= "Murine DPP9 protein"
 FT /note= "CDS does not include start codon"
 FT /partial
 XX
 MO200234900-A1.
 PD 02-MAY-2002
 XX
 PF 29-OCT-2001; 2001MO-AU01388.
 XX
 PR 27-OCT-2000; 2000AU-0001078.
 XX
 PA (UNSW) UNIV SYDNEY.
 XX
 PI Abbott CA, Gorrell MD;
 XX

DR MPI: 2002-454646/48.
DR P-PSDB: AAE24169.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Disclosure: Page 67-70; 91pp: English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immunodeficiency virus) infection. The present
CC sequence is an alternative version of murine DPP9 cDNA.
CC Note: This sequence is stated to be the same as that shown as
CC SEQ ID NO: 3 in Figure 9 of the specification. However these sequences
CC differ.
XX
SO Sequence 3287 BP; 744 A; 970 C; 877 G; 696 T; 0 other;

Alignment Scores:
Pred. No.: 3,52e-279 Length: 3287
Score: 2833.00 Matches: 511
Percent Similarity: 76.79% Conservative: 134
Best Local Similarity: 60.83% Mismatches: 193
Query Match: 60.28% Indels: 2
DB: Gaps: 2

US-10-070-464-1 (1-882) x AAD38955 (1-3287)

QY 35 PheTYrValGluArgTYrSerGluIleuTYrLysLysLeuAlaAspThrArgLys 54
DB 88 TTCTGTGTGCGAGACGACCTGCGGATGGCTGCGTACCATTTACCGAGCGACGCGAAG 147
QY 55 TYrHisGlyTYrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
DB 148 TCTCGGAGGCTCATTTGACGAGGCGCGCCGACGATTCAGTTTGTCAGAACGCTGAC 207
QY 75 ProAspGlyProHisSerAspArgLleTYrTYrLeuAlaMetSerGlyGluAsnArgLys 94
DB 208 GAGTGTGCGCCGACCTGCTACGCTCTATTCCTCGGAAGGCTTACGCGGACGCGTAG 267
QY 95 AsnThrLeuPheTYrSerGluIleProLysThrIleAsnArgAlaValIleuMetLeu 114
DB 268 AACGCTCTCTCTACCTCGAATGCCAAGAAAGTGGGAGAGAGCGCTGCTGCTGCTG 327
QY 115 SerTYrLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTYrGlyMetTYrSerArg 134
DB 328 TCTCGGAGGCTCATTTGACGAGGCGCGCCGACGATTCAGTTTGTCAGAACGCTGAC 387
QY 135 GluIleuGluLeuLeuArgGluArgLysArgLleGlyThrValGlyIleAlaSerTYrAsp 154
DB 388 GAGGAGAGGCTACGCGGAGCGGACGCGCTGCGCTCTTCGGAATCACCCTTTATGAC 447
QY 155 TYrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTYrHisValLys 174
DB 448 TTCCACAGTAGAGCGGCTCTCTCTCCAGGCGAGCATATACCTGTTCCACTGACGAG 507
QY 175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
DB 508 GATGGTGGCAAGATGGCTTATGATGCTCCCGATGAAGCGATGAGATCAAGACTCAG 567
QY 195 CysProAsnIleArgMetAspProLysLeuLysProAlaAspProAspThrIleAlaPhe 214
DB 568 TGTCTGTGGCCACGACGAGACCCAAATATGCCCCCGAGACCTGCTCTTTTCTTCCTC 627
QY 215 IleHisSerAsnAspIleThrIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
DB 628 ATCAACAAGAGTATCTGTGGTGGCAAAACATGACGACTGGGAGGAGAAAGCGGCTCAC 687
QY 235 TYrValHisAsnGluLeuAlaAsnMetGluIleuAspAlaArgSerAlaGlyValAlaThr 254

DB 688 TTCTGTACACGAGGCTTCAGCTGCTCTGACATCCCAATCAGACGCGTGCACAC 747
QY 255 PheValLeuGlnGluIleuPheAspArgTYrSerGlyTYrThrProLysAlaGlu 274
DB 748 TTCTGTATCCAGAGGAGGATTCGACGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGT 807
QY 275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTYrGluGluAsnAspGluSer 293
DB 808 TGGGAGAGCTCCGAAAGGCTTCACAGACGCTCGCATCTATATAGAAAGGAGGAGCTCT 867
QY 294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
DB 868 GAACTGAGGAGCATTCATGTCCTCCCGCCGCTCGAGAGAGAGAGAGAGAGAGAGAG 927
QY 314 ArgTYrProLysThrGlyThrAlaAspProLysValThrPheLysMetSerGluIleMet 333
DB 928 CGCTACCCGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 987
QY 334 IleAspAlaGluGluArgIleLeuAspValIleAspLysGluLeuIleGlnProPheGlu 353
DB 988 ACGGACCATCAGGCGCAAAATCTGTCAAGCTCCAGAAAGAGACGTGATACGCTTACG 1047
QY 354 IleLeuPheGluGluValGluTYrIleAlaArgAlaGlyTYrThrProGluGlyLysTYr 373
DB 1048 TCCCTTTTCCCAAGGAGGAGATCATGCGCGGCTGCTGAGACAGCGAGCGCAATAT 1107
QY 374 AlaThrSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValIleLysSerPro 393
DB 1108 GCGTGGGCGATGTCGTGGAGCGCTCCAGCAAGGCGCTTACGCTTGTCTCTCCCTCT 1167
QY 394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
DB 1168 GCTCTCTTACCCCGCGCGCTTGAAGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGG 1227
QY 414 ProAspSerValThrProLeuIleIleTYrGluGluThrAspIleThrIleAsnIle 433
DB 1228 CCCAAGATGTGCGCCCTTGTCTATGAGAACGATCAACATGCTGTGATCAACGTC 1287
QY 434 HisAspIlePheHisValPheProGluSerHis---GluIleGluIleGluPheIlePhe 452
DB 1288 CAGCAGATCTTCCACCGCTTCTCAGGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGG 1347
QY 453 AlaSerGluLysTYrThrGlyPheArgHisLeuTYrLysIleThrSerIleLeuLysGlu 472
DB 1348 GCCAAGAAATGCAAGACGTGCTTGCACCTGATACAGGATCAAGAGGAACTTAAGAAC 1407
QY 473 SerLysTYrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
DB 1408 AAGGACTATGACTGGAGGAAACCCCTCAGCCCTACAGAGAGTGAAGTTAAGTGCCT 1467
QY 493 LysGluIleIleAlaIleThrSerGlyGluThrProValIleuGluArgHisGlySerAsn 512
DB 1468 AAGGAGAGGCTGCGCTGACAGTGGAGTGGAGGAGTGTGTGTGAGAGCATGGCTTCA 1527
QY 513 IleGlnValAspGluValArgArgLeuValTYrPheGluGluTYrLysAspSerProLeu 532
DB 1528 ATCGGGTCAACAG 1587
QY 533 GluHisHisLeuTYrValValSerTYrValAsnProGlyGluValThrArgLeuThrAsp 552
DB 1588 GAAACATCAGCTATGTCAGTACAGTACAGTACAGGAGAGAGAGAGAGAGAGAGAG 1647
QY 553 ArgLysTYrSerHisSerCysIleSerGlnHisCysAspPheIleSerLysTYr 572
DB 1648 CTGCGCTTCTCCACAGCTGCTCCATGAGCCAGAGCTTCCATATGTCGTGAGTCACT 1707
QY 573 SerAsnGlnLysAsnProHisCysValSerLeuTYrLysLeuSerSerProGluAspAsp 592
DB 1708 AGCAGTGTGAGACAGCGCACCTGTGTACATGTATCAAGCTGAGCGGCGCGAGATGAC 1767
QY 593 ProThrCysLysThrLysGluPheThrAlaThrIleLeuAspSerAlaGlyProLeuPro 612

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Db 1768 CCACTGCAGACAGCAACCCCTTCTGGGCCAGCATGATGAGAGCCCAATTCGCCCA 1827
Qy 613 AsptThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db 1828 GACTATGTGCCCCCTGATCTTCCACTTCCACACCCGTCGACAGCTGCACCTTACGGC 1887
Qy 633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db 1888 ATGATCTACAGACACACACCTTCACACCTGGGAGAGACCCCACTGTGCTCTTGTGTC 1947
Qy 653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db 1948 TATGGGGGCCCAAGGTCAGTGGTGAACACCTCTTAAAGGCATCAATACCTCCCG 2007
Qy 673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db 2008 CTAAATACACTGGCATCTTGGGCTATGCTGTGTGTGATTCGATGGTGGGCTCTGT 2067
Qy 693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db 2068 CACGGGGCTGCTGACCTTCGAGGGGGCCCTGAATAATCAATGGGCCAGTGGAGATTGAG 2127
Qy 713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db 2128 GACCAAGTGAAGAGCTTGCAGTACGTGTCAGAACATGATGCTTCATTTGATTCACCGCA 2187
Qy 733 ValGlyIleHisGlyTyrSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db 2188 GTGGCCATTCATGGCTGTGCTTACGGGGCTTCTCTTCACTCATGGGGCTCATCCACAG 2247
Qy 753 SerAspIlePheArgValAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 772
Db 2248 CCACAGTGTTCAGAGTGAAGCTTGGCGGGCTCTGCTCACTGATGATGATGGCTATGAC 2307
Qy 773 ThrGlyTyrThrGlnArgTyrMetGlnLysProAspGlnAsnGlnGlnGlyTyrLeu 792
Db 2308 ACAGGCTACAGGAGCATCATGATGATGCTCCGAAATATACCAAGCTATAGAGCA 2367
Qy 793 GlySerValAlaMetGlnAlaGlyLysPheProSerGluProAsnArgLeuLeuLeu 812
Db 2368 GGGTGTGTAGCCCTGCATGTGAGAAAGCTGCCCAATGAGCTTAAGCTTATTC 2427
Qy 813 HisGlyPheLeuAspGlnAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
Db 2428 CAGGCTTCCTGACGAGAACGTTCACTTCTCCACAAATTCCTGCTGCCACCTG 2487
Qy 833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGlnArgHisSerIleArg 852
Db 2488 ATCCGAGCAGGAAGCCATATCAGACTTACCCAAACGAGACATATGATCCGC 2547
Qy 853 ValProGluSerGlyGlnHisTyrGlyLeuHisLeuLeuHisTyrLeuGlnGlnAsnLeu 872
Db 2548 TGGCGGAGTCCGGAGAGCATTTAGAGGTGACGCTGTGCACCTTCTGCAGGAACACCTG 2607

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RESULT 22
ABK83339
ID ABK83339 standard; cDNA; 4180 BP.
XX
AC ABK83339;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPRP-2 splice variant #7:
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.

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XX
XX MO200231134-A2.
PN
XX 18-APR-2002.
PD
XX
XX 12-OCT-2001; 2001MO-US31874.
PE
XX
XX 12-OCT-2000; 2000US-240117P.
PR
XX (FERR ) FERRING BV.
PA
XX Q1 S, Akimsanya KO, Riviere PJ, Junien J;
PI
XX WPI: 2002-444178/47.
PT
XX P-PSDB; ABG61608.
PT
XX
XX New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
XX the proteins, useful for treating e.g. fungal, bacterial, protozoan and
XX viral infections, cancers, allergies, neurological disorders, or pain
XX
XX Disclosure: Page 97-98; 113pp; English.
XX
XX The present invention relates to the isolation of novel human serine
XX proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
XX proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
XX and nucleic acids encoding them are useful for treating infections
XX such as fungal, bacterial, protozoan and viral infections, particularly
XX infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
XX pain, diabetes, precocious puberty, infertility, obesity, anorexia,
XX bulimia, Parkinson's disease, acute heart failure, hypotension,
XX hypertension, urinary retention, osteoporosis, angina pectoris,
XX stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
XX psychotic and neurological disorders (e.g. anxiety, dementia, or
XX schizophrenia), and dyskinesias. These may also be used in discovering
XX therapeutic agents for the treatment of reproductive, inflammatory and
XX metabolic disorders. ABK83332-ABK83343 encode human DPRP proteins.
XX
XX
XX Sequence 4180 BP; 898 A; 1312 C; 1178 G; 792 T; 0 other:
XX
XX
XX Alignment Scores:
XX
XX Pred. No.: 9,67e-278 Length: 4180
XX Score: 2820.50 Matches: 510
XX Percent Similarity: 76.43% Conservative: 132
XX Best Local Similarity: 60.71% Mismatches: 183
XX Query Match: 60.01% Indels: 15
XX DB: 24 Gaps: 3
XX
XX US-10-070-464-1 (1-882) x ABK83339 (1-4180)
XX
XX 35 PheTyrValGluArgTyrSerTyrPheSerGlnLeuLysLeuLeuAlaAspThrArgLys 54
XX 436 TTCCAGGTGACAGAGCACTGTGGAGCGGCTCCGGAGCATATCCACGGCAGCGGCAAG 495
XX
XX 55 TyrHisGlyTyrMetAlaLysAlaProHisAspPheMetPheValLysArgAsnArg 74
XX 496 TACTCGGGCCCTCATTTGCAACAGGGCCGCCACACATTCAGATTGGAGAAAGCGAT 555
XX
XX 75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGlnAsnArgGln 94
XX 556 GAGTCTGGGCCCTCCACCTCCACTACTACTGCGAATGCCATATGCGAGCGGAGAG 615
XX
XX 95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaValLeuMetLeu 114
XX 616 AACTCCCTCTTACTTGTGATTTCCCAAGAGGTCGGAAGAGGCTGTGCTCTCTG 675
XX
XX 115 SerTyrLysProLeuAsnAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
XX 676 TCTCGAAGCAGATGCTGATTCATTCACAGGCCACGCCACCATATGGGTACTACTCGG 735
XX
XX 135 GluGlnGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
XX 736 GAGAGAGAGCTGCTGAGAGGAGGAAACGCTGGGCTTTCGCAATCACCTCTTACGAC 795

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155 TyrHisGlnGlySerGlyThrPheLeuPheGlnIleGlySerGlyIleTyrHisValys 174
176 TTCACACGAGGAGTGGCTCTCTCCAGGCGACGACAGCCCTTCCACTGCCG 855
175 AspGlyGlyProGlnGlyPheThrGlnIleProLeuArgProAsnLeuValGlnThrSer 194
856 GACGCGCGCAAGACGGCTCATGTGCTCCATGAACCGCTGGAATACAGACCAG 915
195 CysProAsnIleArgMetLeuAspProGlyLeuGlyProAlaAspProAlaPhe 214
916 TGCACAGGCGCCCGATGAGACCCAAATGCGCCGCGACCTGCTTCTCTCC 975
215 IleHisSerAsnAspIleTyrPheSerAsnIleValThrArgGlnArgArgLeuThr 234
976 ATCATATACAGCAGCTGTGGTGCCAAATCAGACGACGAGGAGGCGGCTGAC 1035
235 TyrValHisAsnGlnLeuAlaAsnMetGlnLeuAspAlaArgSerAlaValAlaThr 254
1036 TTCGCCACCAAGGTTTATCAATGCTCTGGATACCCCAAGTCTGCGGTGCGCCAC 1095
255 PheValLeuGlnGlnIlePheAspArgTyrSerGlyTyrTyrProGlyAlaGln 274
1096 TTCGTCATACAGAGAGATTGACCGCTTCACTGGGTACTGGTGGTCCACAGCCCTCC 1155
275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGlnGlnAsnAspGlnSer 293
1156 TGGGAAGGTTCCAGAGGCGCTCAAGACGCTGCAATCTGTATGAGAGATGATGAGTCC 1215
294 GlnValGlnIleIleHisValThrSerProMetLeuGlnThrArgAlaAspSerPhe 313
1216 GAGGTGGAGGATTCATCACTGCTCTCTGCTGCTAGAAAGAAAGAACAGCGATCGAT 1275
314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGlnIleMet 333
1276 CGGTACCCACAGACAGGACAGAAAGATCCCAAGATGCTTGAAGTGGCTGAGTCCAG 1335
334 IleAspAlaGlnIleArgIleIleAspValIleAspLysGlnLeuIleGlnProPheGln 353
1336 ACTGACACGCGGACAGATGCTCGACCCAGAGAGAGAGAGTGTGACACCCCTTACG 1395
354 IleLeuPheGlnGlnIleValGlnThrIleAlaArgAlaGlyTyrPheProGlnGlyLysTyr 373
1396 TCGGTGTTCCGGAAGGTGATGATACATGCGCAGGCGCGGTGACCGGAGGACCAATAC 1455
374 AlaTyrSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
1456 GCGTGGGCGCATGCTCTGAGACGCGCCACAGAGTGGCTCGTCTCTCTCCCGCG 1515
394 GlnLeuPheIleProValGlnAspAspValMetGlnArgGlnArgLeuIleGlnSerVal 413
1516 GCCCTGTTCATCCGACACAGATGAGAGACGCGCTACGCTTCCGACAGAGCTGTC 1575
414 ProAspSerValThrProLeuIleIleTyrGlnGlnIleThrAspIleThrIleAsnIle 433
1576 CCCGAGATGTCGACCGTATGTGTGATGAGAGGTCACACAGCTGTGATCAATGTT 1635
434 HisAspIlePheHisValPheProGlnSerHis---GlnGlnGlnIleGlnPheIlePhe 452
1636 CATGACATCTCTATCCCTTCCCATCAGAGGAGAGAGACAGCTGTCTTCTCCGCG 1695
453 AlaSerGlnCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGln 472
1696 GCCAATATATGACAGACGCGCTTCTGCCATTGTACAAAGTACACGCGCTTTAAATCC 1755
473 SerLysTyrLysArgSerSerGlyLeuProAlaProSerAspPheLysCysProIle 492
1756 CAGGCGTACGTTGGAGAGACCCCTTACGCGCGGGAAGATGAATTTAACTGCCCATTT 1815
493 LysGlnGlnIleAlaIleThrSerGlyLysArgGlnValLeuGlnArgHisGlySerAsn 512
1816 AAGGAAGAGATGCTGTGACAGCGGTGAATGGAGGTTTGGCGAGGACAGGCTCC--- 1872

513 IleGlnValAspGlnValArgArgLeuValTyrPheGlnGlnIleTyrLysAspSerProLeu 532
1873 -----AAGGCGACCAAGACAGCCGCTG 1896
533 GlnHisIleLeuTyrValValSerTyrValAsnProGlyGlnValThrArgLeuThrAsp 552
1897 GAGCAGCACCTTACAGTCTGACATGACAGCGCGCGGAGAGTGAACGCTTCCACACAG 1956
553 ArgGlyTyrSerHisSerCysHisSerGlnHisCysAspPheIleSerTyr 572
1957 CCGGCTTCTCCATAGCTGCTCAGACGACAGATTCGATGTTGTCAGCAGCTAC 2016
573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGlnAspAsp 592
2017 AGCAGCGTACAGCGCGCGCTGCGTGCATGACAAAGTGAAGCGGCGCCGAGAGAGAC 2076
593 ProThrCysLysThrLysGlnPheThrAlaThrIleLeuAspSerAlaGlyProLeuPro 612
2077 CCGCTGCACAGACGCGCGCTGCGTGAATGATGAGGAGGACGACGCTGCCCGCG 2136
613 AspTyrThrProProGlnIlePheSerPheGlnSerThrThrGlyPheThrLeuTyrGly 632
2137 GATTATGCTCTCCAGAGATCTTCCATTCCACAGCGGCTGATGTCGGCTCTACGCG 2196
633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
2197 ATGATCTACAGACCCCAAGCGCTTGCACGACGAGAAAGACCCACCGCTCTTGTGA 2256
653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
2257 TATGAGGCGCCCGAGGTCACGCTGATGATACCTCTCAAGGACATCACTTGGG 2316
673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgGlySerCys 692
2317 CTCACACAGCGGCTCCCTGCTGCTGACGCGCTGTTGATGATGACGAGGCGCTCTGCT 2376
693 HisArgGlyLeuLysPheGlnGlyAlaPheLysTyrLysMetGlnIleGlnIleAsp 712
2377 CAGCGAGGCTTCGTTGGAAGGCGCTGGAAGGCGCTGGAAGGCGGATGATGAG 2436
713 AspGlnValGlnGlnIleGlnIleTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
2437 GACAGGTGGAGGCTCTGCACTGCTGCGCAGAGATGATGCTTCACTGACCTTACGCGGA 2496
733 ValGlyIleHisGlyTyrSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
2497 GTTGCATCCATGCTGCTGCTACGAGGCGCTTCTGCTGCTCATGAGGCGATATCACAG 2556
753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuThrIlePheTyrAsp 772
2557 CCGCAGGTTCAAGGTGGCCATGCGGCTGCCCGGTCACCGCTGATGCGCTTACGAC 2616
773 ThrGlyTyrThrGlnArgTyrMetGlyHisProAspGlnAsnGlnGlnIleTyrTyrLeu 792
2617 ACAGGATACCTGACCGCTACATGAGCTCCCTAGAACACACGACGCTATGAGCGC 2676
793 GlySerValAlaMetGlnIleGlnLysPheProSerGlnProAsnArgLeuLeuLeu 812
2677 GGTTCGCGGCGCTGCAAGTGGAGACAGCTGCCAATGAGGCCAAGCGCTTCTTATCTC 2736
813 HisGlyPheLeuAspGlnAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
2737 CACGCTTCTCGTGAAGAAAGTGCACCTTTTCCACACAAACTCTCTGCTTCCCACTC 2796
833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGlnIleArgHisSerIleArg 852
2797 ATCCGAGGAGGAAACCTTACACCTCCAGATTAACCCCAAGAGAGACAGATTTCCG 2856
853 ValProGlnSerGlyGlnHisTyrGlnIleuHisLeuLeuHisTyrLeuGlnIleAsnLeu 872
2857 TGCCTCGAGTGGCGGAGACATATGAGTACGTTGCTGCACTTGTACAGAGATTACCTC 2916

RESULT 23

ABR83338
 ID ABR83338 standard; cDNA; 4263 BP.
 AC ABR83338.
 DT 12-AUG-2002 (first entry)
 XX CDNA encoding human DPRP-2 splice variant #6.
 DE
 XX Human: serine protease: dipeptidyl peptidase IV-related protein; DPRP;
 KM DPPY; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KM diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KM heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KM ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KM dyskinesia; reproductive disorder; inflammatory disorder;
 KM metabolic disorder; gene; ss-
 XX
 OS Homo sapiens.
 PN MO200231134-A2
 XX
 PD 18-APR-2002
 XX
 PF 12-OCT-2001; 2001MO-US31874.
 XX
 PR 12-OCT-2000; 2000US-240117P.
 XX
 PA (FERR) FERRING BV.
 XX
 PI Q1 S, Akinsanya KO, Riviere PJ, Juntlen J;
 DR MPI: 2002-444178/47.
 DR P-PSDB: ABG61607.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT
 XX
 PS Disclosure: Page 93-94; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPY)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypertension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABR83322-ABR83343 encode human DPRP proteins.
 CC
 XX
 SQ Sequence 4263 BP; 913 A; 1342 C; 1209 G; 799 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 9,97e-278 Length: 4263
 Score: 2820.50 Matches: 510
 Percent Similarity: 76.43% Conservative: 132
 Best Local Similarity: 60.71% Mismatches: 183
 Query Match: 60.01% Indels: 15
 DB: 24 Gaps: 3
 US-10-070-464-1 (1-882) x ABR83338 (1-4263)
 QY 35 PheTYValGluArgTYrSerGlnLeuLysLysLeuAlaAspThrArgLys 54
 DB 436 TTCCAGTGCAGAACGACGCTGCGAGCGGCTCCGAGCATCATCCAGCGACCGGACG 495
 QY 55 TyHISGlyTYrMetMetAlaLysAlaProHISAspRheMetRheValLysArgAsnAsp 74

DB 496 TACTCGGGCCCTCATTTGCACAAAGCGCCCGACACTTCCAGCTTGTGCAGAGACGAT 555
 QY 75 ProAspGlyProHISSerAspArgIleTYrTYrLeuAlaMetSerGlyGluAsnArgLys 94
 DB 556 GAGTCTGGGGCCCGCCCTCCACCTCCACTACTACTGGAATGTGCATGTGCAGCGGAG 615
 QY 95 AsnThrLeuPheTYrSerGlnIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
 DB 616 AACCTCCCTCTTACTCTGTGAGATTCCACAGAGGTCCGGAAGAGGCTTGTCTCTC 675
 QY 115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTYrGlyMetTYrSerArg 134
 DB 676 TCCGGAAGCAGATGCTGATCATTTCCAGGCCAGCGCCACCATGGGGTACTCTCGG 735
 QY 135 GluGluLeuLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTYrAsp 154
 DB 736 GAGCAGAGCTGCTGAGGAGCGGAAGCGCTGGGCTCTTGGCATCACCCTCTACGAC 795
 QY 155 TyHISGlnGlySerGlyTYrPheLeuPheGlnAlaGlySerGlyIleTYrHISValLys 174
 DB 796 TTCCACAGCGAGCTGCTCTTCTTCCAGGCCAGACAGACCTTCTCCTACCTGCC 855
 QY 175 AspGlyLysProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluTYrSer 194
 DB 856 GACGCGCGCAAGAACGGCTTCATGCTGCCCTTGAACCGCTGGAATCAAGACCCAG 915
 QY 195 CysProAsnIleArgMetLeuAspProLysLeuLysProAlaAspProAspTYrIleAlaPhe 214
 DB 916 TGCTCAGGGCCCGGATGGAGCCCAAAATCTGCTCCCTGCCCTCTTCTCTCC 975
 QY 215 IleHISerAsnAspIleTYrPheSerAsnIleValIleThrArgGluGluArgArgLeuThr 234
 DB 976 ATCATATACACCGACCTGTGGGTGCGCCACATTCAGACAGCGGAGCGGCGCTGAC 1035
 QY 235 TyrValHISasnGluLeuAlaAsnMetGluLysAspAlaArgSerAlaGlyValAlaThr 254
 DB 1036 TTCGACCAAGGATTATCAATGTCGTGATGACCCCAAGTGTGGGGTGGCCACC 1095
 QY 255 PheValIleuGlnGluGluPheAspArgTYrSerGlyTYrTYrPCTPCTProLysAlaGlu 274
 DB 1096 TTCCTCATACAGGAAGGTTGCGACCCCTTCCTGCTGCTAGAGAAAGAGAGGACTCGTAT 1155
 QY 275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTYrGluGluAsnAspGlySer 293
 DB 1156 TGGGAAGCTTCAGAGGGCTTCAGACGCTCGAATCTGTATGAGAGTCAATGATGATCC 1215
 QY 294 GluValGluIleIleHISValIleThrSerProMetLeuGluTYrArgArgAlaAspSerPhe 313
 DB 1216 GAGGTGAGGTCATTCACGTCCTCTCTGCTGCTAGAGAAAGAGAGGAGACTCGTAT 1275
 QY 314 ArgTYrProLysThrGlyThrAlaAsnProLysValIleThrPheLysMetSerGluIleMet 333
 DB 1276 CGGTACCCAGGAGACGACACCAAGATTCCTGTGAATCCGCTGATTCACAG 1335
 QY 334 IleAspAlaGluGluArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
 DB 1336 ACTGACAGCGGACGAGATGCTGTCCAGCCAGGAGAGAGAGCTGTGCAGCCCTTACG 1395
 QY 354 IleLeuPheGluGluValGluTYrIleAlaArgAlaGlyTYrThrProGluGlyLysTYr 373
 DB 1396 TCGCTGTTCGCCGAAGGTGAGATACATCGCCAGGGCCGGGTGAGACCGGATGGCAATATC 1455
 QY 374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
 DB 1456 GCTGGGCGCATGTTCTGTGAGACCGCCAGCAGATGTGCTCCAGCTGCTCTCCCGCC 1515
 QY 394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
 DB 1516 GCCTGTTCATCCGAGACAGAGAAATGAGAGCAGCGGCTAGCCTTGCAGACGCTGC 1575
 QY 414 ProAspSerValThrProLeuIleIleTYrGluGluIleThrThrAspIleTYrIleAsnIle 433

Sequence 2751 BP; 615 A; 820 C; 761 G; 555 T; 0 other;

Alignment Scores:

Pred. NO.:	3_92e-272	Length:	2751
Score:	2763.00	Matches:	508
Percent Similarity:	72.18%	Conservative:	133
Best Local Similarity:	57.21%	Mismatches:	194
Query Match:	58.75%	Indels:	54
DB:	24	Gaps:	3

US-10-070-464-1 (1-882) x AAD38311 (1-2751)

Oy	35	PheYrYalGuIaGuaGyrYrSerTTrSerGlnLeuLysLysLeuLeuAlaAspTrnArgLys	54
Db	89	TTCTGTGGCGAAGAACCTGTGGATGGCTGGTGGACATTATCCACGGCAGTCGCAAG	148
Oy	55	TYrHISgLYrImeTmeAlaLysAlaProHISaspPheMeCPheValLysArgAsnAsp	74
Db	149	TCCTCGGGCCCATTTGTCACAGAGGCCCCACAGACTTCCAGTTTGTGGCAAGACCTGCAC	208
Oy	75	ProAspGlyProHISSerAspArgLIErYrTYrLeuAlaMetSerGlyLuAsnArgLu	94
Db	209	GAGTCGTGGCCCCACTCTCAACCGTCTATTACTCTCGAATGCTTACGGCAGCCCGTAG	268
Oy	95	AsnTrIleuPheTYrSerGlnIleProLysThrLISAsnArgAlaAlaValIleuMetLeu	114
Db	269	AACCTCCCTCTATCTCCGAAATCCCAAGAAATGGGAGGAGGCCCTGCCTGCTG	328
Oy	115	SerTrpLysProLeuLeuAspLeuPheGlnAlaTrhLeuAspTYrGlyImeTYrSerArg	134
Db	329	TCCTGGAGACGATGCTGTGCACACTTTCAGGCCACACCACCTGGTGTCTACTCCGA	388
Oy	135	GluGluGluLeuLeuAsnArgLuArgLysArgLIEGLYrThrValGlyLIEAlaSerTYrAsp	154
Db	389	GAGAGGAGCTACTGCGGGAGCCCAAGCCGCTGGCGCTTCGGAATCACCTCTATGAC	448
Oy	155	TYrHISgInGlySerGlyThrPheLeuPheGlnAlaGlySerGlyLIErYrHISValLys	174
Db	449	TTTCAACGTGAGACCGGCTCTTCTCTTCCAGGCCAGCAATACCCGTTCACCTGCAG	508
Oy	175	AspGlyGlyProGInGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer	194
Db	509	CATGCTGGCAAGATGGCTTTATGTGTCTCCCGATGAAGCACCTGGAGATCAAGACTCAG	568
Oy	195	CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe	214
Db	569	TGTTCTGGGCCACCATGGAGACCCCAAAATGTGCCCGCAGACCCTCTTTTCTTCTTC	628
Oy	215	IleHISerAsnAspLIErTrpLIESerAsnIleValThrArgGluGluArgArgLeuThr	234
Db	629	ATCAACAACACTGTATCTGTGTGGCAACACTGGGGGAGGAACGGCGCTCACCC	688
Oy	235	TYrAlaHISAsnGluLeuAlaAsnMeGluGluAspAlaArgSerAlaGlyValAlaThr	254
Db	669	TTCTGTCAACCGGTTCACTGCTGTCTCTGGACATATCCCAATGAGAGCGTGGCCACC	718
Oy	255	PheValLeuGInGluGluPheAspArgTYrSerLIErTYrTrpCysProLysAlaGlu	274
Db	749	TTTGTCAATCCAGGAGGATTCGACCGCTTCACTGTGGTGGTGGTGGTGGCCACAGCGCTT	808
Oy	275	ThrTrpProSerGlyGly--LysIleLeuArgLIELeuTYrGluGluAsnAspGluSer	293
Db	809	TGGGAGAGCTCCGAAGTCTTCMAAGCTCGGTGCATCTTATATGAGGAAGTCAGAGACTT	868
Oy	294	GluValGluIleIleHISValThrSerProMetLeuGlnThrArgArgAlaAspSerPhe	313
Db	869	GAGGGAGGCTATTCATGTGCTCCCTCCCGCCCTGGAGGAGAGCAAGACGACTCTTAC	928
Oy	314	ArgTYrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet	333
Db	929	CGCTACCCCGAGACAGGAGCAAAACCCCAAGTATGCTCGAAGCTGGCTGACCTCAG	988
Oy	334	IleAspAlaGluGlyArgGlyLIEAspValIleAspLysGluLeuIleGlnProPheGlu	353

Db	989	ACGGACATCAGGGCAAAATCGTGCACCTGCGAGAAAGCAACTGTGTACAGCAATTCAAC	1048
Oy	354	lLeaulepHeugluGluValGluTYrIleAlaArgAlaGlyrPrThrProGluLysTYr	373
Db	1049	TCCCTTTTCCCAAGAGGAGTACATCGCCGGGCTGGCTGGACACGGAGCGCAAAATAT	1108
Oy	374	AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro	393
Db	1109	GCGTGGGCGCATGTTCCTGGAGCCGTGCCACAAAGCGGCTTTCACCTTGTCTCTCGCCCT	1168
Oy	394	GluLeuPheIleProValIguAspAspValMetGluArgGlnArgLeuIleGluSerVal	413
Db	1169	GCTCTTTCATCCGGCGGCTTGGAGTGAAGCCACCGGCGAGGACCTGGCAGAGCCCTC	1228
Oy	414	ProAspSerIleThrProLeuIleIleTYrGluGluThrThrAspIlePrIleAsnIle	433
Db	1229	CCCAAGAAATGGCAGCCCTTGTGCATCTATGAAGAAGTCCACAAATGTCTGATCAACCTC	1288
Oy	434	HisAspIlePheHisValPheProGlnSerHis--GluGluGluIleGluPheIlePhe	452
Db	1289	CACACATCTTCCACCCGTTTCCCTCAGGGCTGAAGGGCCACAGACAGATTTGTGTTCTTCTG	1348
Oy	453	AlaSerGluCysLysTrpArgIlePheArgHisLeuTYrIleThSerIleLeuLysGlu	472
Db	1349	GCCACAGAAATGCAAGACTGCTTCTGCCACCTGTACAGGGTACAGGTGAATTAAC	1408
Oy	473	SerTYrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle	492
Db	1409	AAGACATGTACTGACGAGCAACCCCTCACCCCTACAGAAAGTGAGTTAAGTCCCATC	1468
Oy	493	LysGluGluIleAlaIleThrSerGlyGluTYrPglValLeuGlyArgHisGlySerAsn	512
Db	1469	AAGAGAGAGGTCCGCTGACACAGTGGCGAGTGGAGAGTCTTGTCCAGGCATGCTCCACAG	1528
Oy	513	IleGlnAlaAspGluValArgArgLeuValTYrPheGluGlyThrLysAspSerProIle	532
Db	1529	ATCTGGGTCAACGAGCAGACGAAGCTGGGTGTACTTTCAGAGTACAAAGACACACCCCTG	1588
Oy	533	GluHisHisLeuTYrValAlaSerTYrValAsnProGluGluValAlaThrArgLeuHisAsp	552
Db	1589	GAACATCACCTTATGTGTGTGCTACCTACAGATCAGACGGGAGACATCGTGGCGTCAACAG	1648
Oy	553	ArgGlyTYrSerHisSerCysLysIleSerGlnHisCysAspPhePheIleSerLysTYr	572
Db	1649	CTCGGCTTCTCCACACTGCTCTCATAGAGCAGAGCTTGACATGTGCTGGTACCTATAC	1708
Oy	573	SerAsnGlnLysAsnProHisCysValSerLeuTYrLysLeuSerSerProGluAspAsp	592
Db	1709	AGCAGGTGAGACGACGACCCCTGTGTACATGTGTACAACTAGAGCGGCCCATATGATAC	1768
Oy	593	ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro	612
Db	1769	CCACTGCACAAAGCAACACACCTTCTGGGCCAGAGTATGAGAGCAACCAATTGGCCCCCA	1828
Oy	613	AspTYrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTYrGly	632
Db	1829	GACTATGTGCCCCCTGTGATCTTCCACTTCCACACCGGTGACAGAGCTGACCTTAAGCGC	1888
Oy	633	MetLeuTYrLysProHisAspLeuGlnProGlyLysLysTYrProThrValLeuPheIle	652
Db	1889	ATGATCTTACAAAGCCACACACCTGTCAACCTGGAGAGAACACCCCACTGTGCTTTTTC	1948
Oy	653	TYrGlyGlyProGlnValGlnLeuValAsnAspArgPheLysGlyValLysTYrPheArg	672
Db	1949	TATGGGGCCCAACGGGCGAGTTGGTGGTAACTCTTTAAAGGCACTCAAAATACCTGGCG	2008
Oy	673	LeuAsnThrLeuAlaSerLeuGlyTYrValValValValIleAspAsnArgGlySerCys	692
Db	2009	CTAATATACAGCGGATCTTGGGCTATGCTGTGTGTATATGATGATGTCGGGCTCCCTGT	2068
Oy	693	HisArgGlyLeuLysPheGluGlyAlaPheLysTYrLysMetCylGlnIleGluIleAsp	712

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Db 2069 CAGCGGGGCTGCACCTTCGAGGGGCCCCGAAATCAATGGCCAGGTGAGATTGAG 2128
QY 713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db 2129 GACCAAGTGGAGAGCTTCGACATGCTGCTGAGAAAGTATGCTTCACTTACCTAGCCGA 2188
QY 733 ValGlyIleHisGlyTyrPheTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db 2189 GTCCACATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2248
QY 753 SerAspIlePheArgValAlaIleAlaGlyValProValTyrLeuTyrPheTyrAsp 772
Db 2249 CCACAGAGTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2308
QY 773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
Db 2309 ACAGAGTACACGAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2368
QY 793 GlySerValAlaMetGlnAlaGlyLysPheProSerGluProAsnArgLeuLeuLeu 812
Db 2369 GGGCTGTAGCCCTGCATGTGTGAGAGACCTGCCAATGAGCTTAACCCCTCTTATCTCTC 2428
QY 813 HisGlyPheLeuAspGluAsnValHisPheIleHisThrSerIleLeuLeuSerPheLeu 832
Db 2429 CACGGCTTCCTGAGACGAGAACGTTCACTTCTCCACACAAATTTCTGTGTCTCCAGCTG 2488
QY 833 ValArgIleGlyLysProTyrAspLeuGlnIle----- 843
Db 2489 ATCCGACAGAGAAAGCCATACACCTTCAGGT-TGCATCATGTCACAAACCTCACTGACT 2547
QY 843 ----- 843
Db 2548 ACCCTCACTAAGACCCAGTTTGTATGAACCCACTTGGCTACAGCATGGAGAGTGCCTCC 2607
QY 843 ----- 843
Db 2608 CCAATGATTTAGAGACCCAAAGACGACTTGGCTGAGGAGAGACATTTAAAGCTCCAGAGAC 2667
QY 844 -----TyrProGlnGluArgHisSerIleArgValProGlnSerGlyGlnHisTyrGlu 861
Db 2668 TGAATCATACCAAAAGAGACATACATCCGCTGCGCGAGAGTCCGGAGACATTAAGAG 2727
QY 862 LeuHisLeuLeuHisTyrLeuGln 869
Db 2728 GTGACGCTGCTGCACCTTCTGACG 2751

RESULT 25
ABK83337
ID ABK83337 standard; cDNA; 4076 BP.
AC ABK83337:
XX
XX 12-AUG-2002 (first entry)
DT
XX
DE cDNA encoding human DPRP-2 splice variant #5.
XX
XX Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
XX DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
XX diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
XX heart failure; hypertension; urinary retention; osteoporosis; cancer;
XX ulcer; allergy; cancer; psychotic disorder; neurological disorder;
XX dyskinnesia; reproductive disorder; inflammatory disorder;
XX metabolic disorder; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200231134-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001MO-US31874.
XX
XX 12-OCT-2000; 2000US-240117P.
XX
XX
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XX
XX (FERR ) FERRING BV.
PA
XX Q1 S, Akinsanya KO, Riviere PJ, Junien J;
PI
XX WPI; 2002-444178/47.
DR
XX P-PSDB: ABG61606.
DR
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT
XX
PS Disclosure; Page 90-91; 113pp; English.
XX
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinasias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
XX
SQ Sequence 4076 BP; 879 A; 1276 C; 1143 G; 778 T; 0 other:

Alignment Scores:
Pred. No.: 3,36e-260 Length: 4076
Score: 2649.00 Matches: 485
Percent Similarity: 72.89% Conservative: 127
Best Local Similarity: 57.79% Mismatches: 177
Query Match: 56.36% Indels: 51
DB: 24 Gaps: 3

US-10-070-464-1 (1-882) x ABK83337 (1-4076)
QY 35 PheTyrValGluArgTyrSerTyrPheSerGlnLeuLysLysLeuAlaAspThrArgLys 54
Db 436 TTCACGGTGGAGAGACATGCTGGAGCGGCTCCGGAGCATCAACCCAGCGCAGCGAG 495
QY 55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheValLysArgAsp 74
Db 496 TACTCGGGCTCATTTGTCACAAAGCGCCGCCACGACTTCCAGTTGTGCGAGAACGCGAT 555
QY 75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
Db 556 GAGTCTGGGCGCCATGTCACAAAGCGCCGCCACGACTTCCAGTTGTGCGAGAACGCGAT 615
QY 95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
Db 616 AACCTCCCTCCTCTACTCTGAGATCCCAAGAGAGTCCGGAAGAGCTGCTGCTCTCTG 675
QY 115 SerTyrLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
Db 676 TCCGGAAGAGAGATGTCATTCACAGGCGCCAGCCCACTGGGCTGCTACTCTCGG 735
QY 135 GlnGlnGlnLeuLeuAspArgGluArgGlyIleGlyTyrValGlyIleAlaSerTyrAsp 154
Db 736 GAGAGAGAGCTGTCAGAGAGCGAAGCGCTGGGGCTTTCGSCATACACTCTCTAGAC 795
QY 155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaIleArgSerGlyIleTyrHisValLys 174
Db 796 TTCACAGCAGAGAGTGGCTTCTCTCCAGGCGCAGCAACACCTCTCCACTGCGCG 855
QY 175 AspGlyGlyProGlnGlnPheThrGlnGlnProLeuArgProAsnLeuValGlnTyrSer 194
Db 856 GACGCGGCAAGAACGCTTCATGCTGCTCCCTATGTAACCGCTGGAAATCAAGACCCAG 915
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195 CysProAsn1LeuArgMetAspProLysLeuCysProAlaAspProAspThrIleAlaPhe 214
 916 TCGTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCTCCCTTCTCTTC 975
 215 1LeuHisSerAsnAspIleThrIleSerAsn1LeuValThrArgGluGluArgArgLeuThr 234
 976 ATCAATTAACAGGACCTGTGGTGGCCACATCGAAGCAGGAGGAGGCGGGCTGACC 1035
 235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerIleAlaValAlaThr 254
 1036 TTCTGCCACCAAGATTATTCATGTCTGGATGACCCCAAGTCTGGGTGGCCACC 1095
 255 PheValLeuGluGluGluPheAspArgTyrSerGlyTyrThrProCysProLysAlaGlu 274
 1096 TTGCTCATACAGGAAGATTCACCCCTTCACTGGGTACTGGGTGGCCCAAGCTCC 1155
 275 ThrThrProSerGlyGly--LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
 1156 TGGGAAGTTTCAGAGGGCTCAAGAGCTGCGAATCTGTATGAGCAAGTCTGTAGTCC 1215
 294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
 1216 GAGGTGAGAGTATTACATCTCCCTCTCGCTAGAAAGAAAGAGAGAGAGCTGTAT 1275
 314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
 1276 CGGTACCCAGGACAGGACGCAAAATCCCAAGATTGCTTGAATGGCTGAGTTCAG 1335
 334 1LeuAspAlaGluGlyArgIleIleAspVal1LeuAspLysGluLeuIleGluProPheGlu 353
 1336 ACTGACAGCAGGAGGAGATGCTCGACCCAGGAGAGAGAGCTGTGACGCTTCACG 1395
 354 1LeuPheGluGluGlyValGluTyrIleAlaArgAlaGlyThrPheProGluGlyLysTyr 373
 1396 TCGCTTCTCCCAAGGTGAGATGATGCCAGAGGCGGGTGGACCGGGATGGCAATAC 1455
 374 AlaIlePheIleLeuLeuAspArgSerGluThrArgLeuGlu1LeuValLeuIleSerPro 393
 1456 GCGTGGCCATGTCCTGTGACCGGCGCCAGCATGGCTCTCAGCTGCTCCCTCCGCCG 1515
 394 GluLeuPheIleProValGluAspAspValMetGluArgGluArgLeuIleGluSerVal 413
 1516 GCCGTGTTATCTGCGACAGCAAGATGAGAGACGCGCTACGCTCCAGAGCTGTC 1575
 414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleThrIleAsnIle 433
 1576 CCCAGGAATGTCAGCCGATGTGTGTACGAGAGAGTCAACAGCTGTGATCAATGTT 1635
 434 HisAspIlePheHisValPheProGluSerHis--GluGluGluIleGluPheIlePhe 452
 1636 CATGACATCTGTATCCCTCCCCCAATCAGAGGAGAGAGAGAGCTGCTTCTCCCG 1695
 453 AlaSerGluCysLysThrLysPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
 1696 GCCAATGAATGGAAGACCGGCTTGTGCAATTTGTACAAAGTCAACCCCTTTTAAATCC 1755
 473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
 1756 CAGGGTACGATTGGAGTAGCCCTTCAAGCCCGGGGAAGATTAATTTAAGTCCCAATT 1815
 493 LysGluGluIleAlaIleThrSerGlyGluTyrGluValLeuGlyArgIleGlySerAsn 512
 1816 AAGGAAGAGATGTCCTGACCAAGCGGTGAATGGAGGTTTGGCCAGGACGCTCCAG 1875
 513 1LeuGluValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
 1876 ATCTGGGTCAATGAGAGCAACAGCTGTACTTCCAGGGCCCAAGAGACAGCGCGCTG 1935
 533 GluHisIleLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
 1936 GAGCACCACTCTACGTGGTCACTATGAGGCGGCGGAGATGCTACGCTCACACAGC 1995

553 ArgGlyTyrSerHisSerCysCysIleSerGluHisCysAspPheIleSerLysTyr 572
 1996 CCGGCGTCTCCATAGCTGCTCCATGACCCAGAACTTGACATGTCTGACAGCCATAC 2055
 573 SerAsnGluLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
 2056 AGCAGCGTACAGCCGCCGCTGCGTGCAGACGTCATCAAACTGAGCGGCCGCGACAGC 2115
 593 ProThrCysLysThrLysGluPheThrPheIleIleLeuAspSerIleAlaGlyProLeuPro 612
 2116 CCGTTCACAGAGAGCCCGCTTCTGCTAGCATGATGAGGACAGCAGCTGCCCGCCG 2175
 613 AspTyrThrProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
 2176 GATTATGTCCTCCATAGATCTTCATTCATCCACAGCGCTCGGATGCGGCTCTACGGC 2235
 633 MetLeuTyrLysProHisAspLeuGluProGlyLysLysTyrProThrValLeuPheIle 652
 2236 ATGATCTACAGCCCGCCGCTTGCAGCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2295
 653 TyrGlyGlyProGluValGluLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
 2296 TATGAGAGCCCGCCAGGTGAGCTGTGATTAATCTCTTCAAGGCAATCAAGTATGCGG 2355
 673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgLysSerCys 692
 2356 CTCACACACATGGCCCTCCGCGGCTACGGCGTACGGCTGTGATTCAGAGGAGCGCTCTG 2415
 693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGluIleGluIleAsp 712
 2416 CAGCGAGGCTTGGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2475
 713 AspGluValGluGlyLeuGluGluThrAlaSerArgTyrAspPheIleAspLeuAspArg 732
 2476 GACCAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2535
 733 ValGlyIleHisGlyTyrPheTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGluArg 752
 2536 GTTGGCATCATGGTGTGTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2595
 753 SerAspIlePheArgValAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAla 772
 2596 CCCCAGGTGTTCAGG----- 2611
 772 PthrGlyTyrThrGluArgTyrMetGlyHisProAspGluAsnGluGlyTyrTyrLe 792
 2611 ----- 2631
 792 uGlySerValAlaMetGluAlaGluLysPheProSerGluProAsnArgLeuLeuLeu 812
 2612 -----CCCAACCGGTGCTTATCC 2631
 812 uHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLe 832
 2632 CCACGGCTTCTGAGAAACGTGCACTTTTCCACAAACTTCTGCTGCCCAACT 2691
 832 uValArgAlaGlyLysProTyrAspLeuGluIleTyrProGluGluArgHisSerLeu 852
 2692 GATCCAGCAGGAGAAACCTTACAGCTCCAGATCTACCCCAAGAGAGACAGACTTTGG 2751
 852 gValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGluGluAsnLe 872
 2752 CTCGCCGAGTGGGAGAGACATGAGTACAGCTTGTGCACTTTCTACAGAAATACCT 2811
 872 u 872
 2812 C 2812
 RESULT 26
 ABR83336
 ID ABR83336 standard; cDNA; 4159 BP.
 AC ABR83336;

XX	12-AUG-2002	(first entry)	
XX			
DE	cdna encoding human DPPP-2 splice variant #4.		
XX			
XX	Human; serine protease; dipeptidyl peptidase IV-related protein; DPPP;		
KW	DPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;		
KW	diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;		
KW	heart failure; hypertension; urinary retention; osteoporosis; cancer;		
KW	ulcer; allergy; cancer; psychotic disorder; neurological disorder;		
KW	dyskinesia; reproductive disorder; inflammatory disorder;		
KW	metabolic disorder; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200231134-A2.		
XX			
PD	18-APR-2002.		
XX			
XX	12-OCT-2001; 2001WO-US31874.		
PF			
XX	12-OCT-2000; 2000US-240117P.		
XX			
PR	(FERR) FERRING BV.		
PA			
PI	Qi S, Akinsanya KO, Riviere PJ, Junien J;		
XX			
DR	WPI; 2002-444178/47.		
XX	P-PSDB; ABG61605.		
XX			
PT	New dipeptidyl peptidase IV-related proteins and nucleic acids encoding		
PT	the proteins, useful for treating e.g. fungal, bacterial, protozoan and		
PT	viral infections, cancers, allergies, neurological disorders, or pain		
PT			
PS	Disclosure; page 87-88; 113pp; English.		
XX			
CC	The present invention relates to the isolation of novel human serine		
CC	proteases referred to as dipeptidyl peptidase IV (DPIV)-related		
CC	proteins (DPPP). The dipeptidyl peptidase IV-related proteins (DPPP)		
CC	and nucleic acids encoding them are useful for treating infections		
CC	such as fungal, bacterial, protozoan and viral infections, particularly		
CC	infections caused by human immunodeficiency virus (HIV-1 or HIV-2),		
CC	pain, diabetes, precocious puberty, infertility, obesity, anorexia,		
CC	bulimia, Parkinson's disease, acute heart failure, hypotension,		
CC	hypertension, urinary retention, osteoporosis, angina pectoris,		
CC	stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,		
CC	psychotic and neurological disorders (e.g. anxiety, dementia, or		
CC	schizophrenia), and dyskinesias. These may also be used in discovering		
CC	therapeutic agents for the treatment of reproductive, inflammatory and		
CC	metabolic disorders. ABR83322-ABR83343 encode human DPPP proteins.		
XX			
SO	Sequence 4159 BP; 894 A; 1306 C; 1174 G; 765 T; 0 other;		
	Alignment Scores:		
	Pred. NO: 3,46e-260	Length: 4159	
	Score: 2649.00	Matches: 486	
	Percent Similarity: 72.89%	Conservative: 127	
	Best Local Similarity: 57.79%	Mismatch: 177	
	Query Match: 56.36%	Indels: 51	
	DB: 24	Gaps: 3	
	US-10-070-464-1 (1-882) x ABR83336 (1-4159)		
Oy	35 PheTYValAlGluArgTYSerTTPserGlnLeuLYsLYsLeuLeuAlaAspPhrArgLYs 54		
	: : : :		
Db	436 TTCCAGGTGCAACACCTCGTGGAGCGGCTCCGGACATATCATCCAGCGCCGCAAG 495		
	: : : :		
Oy	55 TYrHsGlyTYrMetMetAlaLYsAlaProHISAspPheMetPheValLYsArgAsnSP 74		
	: : : :		
Db	496 TACTCGGGGCGTCATGTGTGCACAAAGCGCCGCCACGACTTGTGTGCAGAAAGCGAT 555		
	: : : :		
Oy	75 ProAspGlyProHISerAspArgIleTYrTYrLeuAlaMetSerCylGluAsnArgGlu 94		

Db	556	GAGTCGTGGGCCCCCACTCCACACCGCTCTACTACTCGGAATGCATATGACAGCCAGGAG	615
Oy	95	AsnThrLeuPheTyrSerGluIleProIlyrThrIleAsnAlaAlaValLeuMetLeu	114
Db	616	AACCTCCCTCTACTCTGTGAGATTCCCAAGAGTCCGGAAGAGAGCTCTGCTGCTCTG	675
Oy	115	SerTrpIlyrProLeuIleAsnAlaPheGlnAlaThrLeuAspTyrGlyMetLeuSerArg	134
Db	676	TCCTGGAAAGCAGATGCTGTGATTCATTTCACAGCCACGCCCCACCATTGGGGTCTACTCTGG	735
Oy	135	GluGluGluLeuLeuAsnArgGluArgIyAsnGlyIleGlyThrValGlyIleAlaSerTyrAsp	154
Db	736	GAGCAGAGCGCTGTGAGAGGAGCGGAAACGCGCTGGGGCTTCCGCGATCCCTCTACAC	795
Oy	155	TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIlePheHisValys	174
Db	796	TTTCCACACCGAGATGGCTCTTCTCTTCCAGGCGACGACAGACCTCTTCCACTGCGCC	855
Oy	175	AspGlyIlyrProGlnGlyPheThrGlnGlnProLeuAsnProAsnLeuValGluThrSer	194
Db	856	GACGGCGGCAAGACGGCTTCATGGTGTGCCATGAAACCGCTGGAAATCAAGACCCAG	915
Oy	195	CysProAsnIleArgMetAspProIlyrLeuCysProAlaAspProAspTrpIleAlaPhe	214
Db	916	TGCTCAGGGCCCCGGAATGGAGCCCAAAATCTGGCCCGCGACCTCCCTTCTTCTCTTC	975
Oy	215	IleHisSerAsnAspIleTyrPheSerAsnIleValThrArgGluGluArgArgLeuThr	234
Db	976	ATCATATACACAGCACCTGTGGGTGGCCACATGTGAACACAGGAGAGGCGGCGCTGAC	1033
Oy	235	TyrValHisAsnGluLeuAlaAsnMetGluAsnAspAlaArgSerAlaGlyAlaThr	254
Db	1036	TTTCTGCCACCAAGGTTTATTCCAATGTCTCTGGAGACCCCAAGCTCTCGGGTCTGGCCAC	1095
Oy	255	PheValLeuGlnGluGluPheAsnArgTyrSerGlyTyrTyrTrpCysProIlyrAsnGlu	274
Db	1096	TTCTGCTATACAGAGAGAGTTCTGACCGCTTACTGGGTACTGGTGTGGCCCAACACTCC	1155
Oy	275	ThrThrProSerGlyGly--LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer	293
Db	1156	TGGGAGAGTTCTAGAGGCGCTTCAGACGCTCGAATCCTGTATAGAGAACTCATATGATCC	1215
Oy	294	GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe	313
Db	1216	GAGGTGGAGGTCAATTCACGTCCTCTCCGCGCTGAAAGAAAGGAAGACGCACTCGTAT	1275
Oy	314	ArgTyrProIlyrThrGlyThrAlaAsnProIlyrValThrPheIlyrMetSerGluLeuMet	333
Db	1276	CGGTACCCCGACAGACAGCAGACAGAATCCCAAGATTGCTTGAAACTGGCTGATTTCCAG	1333
Oy	334	IleAsnAlaGluGlyArgIleIleAsnValIleAsnIlyrGluLeuIleGlnProPheGlu	353
Db	1336	ACTACACAGCCGAGGCAAGATCGTCTGCACCCAGCAAGAGAGATGGTGTGACGCTTTCAC	1395
Oy	354	IleLeuPheGluGluValGluTyrTyrIleAlaArgAlaGlyTyrThrProGluGlyIlyr	373
Db	1396	TCGCTGTTCGGAAGGTGGAGTACATGCCAGGAGCGGGGTGGACCCGGATGTGCAATATAC	1455
Oy	374	AlaTrpSerIleLeuLeuAsnAspArgSerGlnThrArgLeuGlnIleValIleuIleSerPro	393
Db	1456	GCTGTGGGCATGTCTGTGACCGGCCCCACACAGATGGCTCTCAGCTGTCTCTCTCCCCCG	1515
Oy	394	GluLeuPheIleProValGluAsnAspValMetGluArgGluArgLeuIleuIleuSerVal	413
Db	1516	GCCCTGTTCATCCCGACACAGAGATGAGAGACACCGCTGTACCTTCCAGACTGTTC	1575
Oy	414	ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle	433
Db	1576	CCGACGAAATGTCCACCGCTATGTGTGTCTACAGAGAGCTCACACAGCTGTGATCATATGTT	1633
Oy	434	HisAspIlePheHisValPheProGlnSerHis--GluGluGluIleGluPheIlePhe	452

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Db 1636 CATGACATTTTATTCCTCCCTCCCAATCAGAGGAGGAGGAGCTGCTTCTCCGC 1695
QY 453 AAlaserGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
Db 1696 GCCAATGAAATGACAGACCGGCTTCCTGCAATTTGTACAAAGTCACCGCCGCTTTAAATGC 1755
QY 473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
Db 1756 CAGGCTACGATTTGAGTACGAGCCCTTCAGCCCGGGAAGATTTTAAGTGCCTCATTT 1815
QY 493 LysGluGluIleAlaIleThrSerGlyGlyTyrPglIuValLeuGlyArgHisLysSeran 512
Db 1816 AAGGAAGAAATGCTCTGCTCCAGCGGTGAATGAGAGTTTTCGCGAGCAGCGCTCCAG 1875
QY 513 IlegInValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
Db 1876 ATCTGGGTCAATGAGAGACACCAAGCTGGTACTTCCAGGACACAGACAGCGCCGCTG 1935
QY 533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
Db 1936 GAGCACACCTCTACGTGCTACGTATGAGCGCGCGGAGATGCTACGCTCCACACAG 1995
QY 553 ArgGlyTyrSerHisSerCysLysLeuSerGlnHisCysAspPhePheIleSerLysTyr 572
Db 1996 CCGGCTCTCTCCATAGCTGCTCCATGAGCCAGACTTCCATGATGTTGCTGACCCACTAC 2055
QY 573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAsp 592
Db 2056 ACCACGCTGAGACAGCGCGGCTCGGTCACGCTACCACTACAGCGCGCCGACGACGAC 2115
QY 593 ProThrCysLysThrLysGluPheThrPalThrIleLeuAspSerAlaGlyProLeuPro 612
Db 2116 CCCCACACACACACACACCGCTCTGCGGTACAGATGAGAGCAGCCAGCTGCCCGCG 2175
QY 613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db 2176 GATTATGCTCTCCAGAGATCTTCCATTTCCACAGCGCTCGGATGCTCGGCTCTGAG 2235
QY 633 MetLeuTyrLysProHisAspLeuGlnProGlyLysTyrProThrValLeuPheIle 652
Db 2236 ATGATCTACAAACCCCGACGCTTCGACGCCAGGAGAAACACCCCGCTCTCTGTA 2295
QY 653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db 2296 TATGAGAGCCCGCCAGGTGACGTGATTAATCTCCAAAGCATCAAGTACTGCGCG 2355
QY 673 LeuAsnThrLeuAlaSerLeuGlyTyrValValIleValIleAspAsnArgLysCys 692
Db 2356 CTCACACACCTGCTCCCTGGGCTACGCCGTGCTGATTGACGCGCAGGGGCTCTGT 2415
QY 693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db 2416 CAGCGAGGCTTCGGTTCGAAAGGCGCCGCAAAACCAATGGCCAGCTGAGATCGAG 2475
QY 713 AspGlnValGluGlyLeuGlnIleTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db 2476 GACCAAGGTGAGCGCTGCTGCTGCGCGCAGAGTATGCTTCATCGACCTGAGCGCA 2535
QY 733 ValGlyIleHisGlyTyrSerTyrGlyGlyTyrLysSerLeuMetAlaLeuMetGlnArg 752
Db 2536 GTTGCATTCACATGCTGCTGCTACGAGGCGCTTCCTGCTCATGGGCTTAATCCACAAG 2595
QY 753 SerAspIlePhe-ArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAs 772
Db 2596 CCCAGAGGTTCAGG----- 2611
QY 772 PThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLe 792
Db 2611 ----- 2611
QY 792 uGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeu 812
Db 2612 -----CCCAACCGGCTCTTATCT 2631

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QY 812 uHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLe 832
Db 2632 CCACGGCTTCCTGAGAGAAACGTCACCTTTTCCACACAAACTTCCTGCTCCCAACT 2691
QY 832 uValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleAr 852
Db 2692 GATCCGAGCAGGAGAAACCTTACACGCTCCGATCTTACCCCAAGAGACACAGTATTCG 2751
QY 852 gValProGluSerGlyGlnHisTyrGluGluHisLeuLeuHisTyrLeuGlnGluAsnLe 872
Db 2752 CTGCCCCGATGCGGCGAGCAGTGAAGTCACTGCTGCACTTTCACAGGAATACCT 2811
QY 872 u 872
Db 2812 C 2812

RESULT 27
AA157896
AA157896 standard; cDNA; 2801 BP.
ID
AC AA157896;
XX
XX 22-OCT-2001 (first entry)
DE
XX Human polynucleotide SEQ ID NO 99.
XX
XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia; ss.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX
XX 25-APR-2000; 2000US-0552317.
XX
XX 09-JUL-2000; 2000US-0598042.
XX
XX 19-JUL-2000; 2000US-0620312.
XX
XX 03-AUG-2000; 2000US-0653450.
XX
XX 14-SEP-2000; 2000US-0662191.
XX
XX 19-OCT-2000; 2000US-0693036.
XX
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D:
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao Q, Zhou P, Goodrich R, Drmanac RT;
XX
XX MPI: 2001-442253/47.
XX P-PSDB: AAM38740.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX
XX Claim 1: SEQ ID NO 99; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX CC the encoded polypeptides (AAM38642-AA42213) with nootropic,
XX CC immunosuppressant and cyostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localized neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

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D	b		GCACCCACCCTCCTTTTGTATATGAGAGCCCCCAGGTGCAGCGTGGAATAACTCCTT	2149
Oy		665	eLysGIYValIlystYrPheArLeuAsnThrIeuaIaserLeuGIYrValValVa	685
D	b	2150	CAAAAGCATCAAGTACTTCGGCGCTCAACAACACTGGCGCTCCCGGGCTACGCCGTGGTGT	2209
Oy		685	IleAsPAsrArgISerCySHisrgrIyeuLysPheGIuGLyaIaphelysTyTLy	705
D	b	2210	GATTGACGCGAGAGGGCTCCCTGATGCGAGGGCTTCGGTTCAAGGGGGCCCTGAAAACCA	2269
Oy		705	smeGIyGLInIleGLuILeasPaspeINalGLuGLyeuGLNTrLeuaIaserArty	725
D	b	2270	AATGGCCAGCGTAGAGATCGAGAGCACAGGTGAGGGCCTCGAGTTGCGGCCAGAAGTA	2329
Oy		725	rAsPPhIIAsPLeuAsPaRgValIdLyIlenIsGLYTPserTYrGIyGLYTyrLeuSe	745
D	b	2330	TGGCTTATGACCTGAGCGGCAATTCSCATCCATGAGGTGGTCTACGGGGGCTTCCTTC	2389
Oy		745	rLeueAlaleuMetoLIuNrSerAsPIIlePheArGValAIAlIleAlaIylAProVa	765
D	b	2390	GCCTATGGGGCTAATCCACAAAGCCCAGGTGTCAAAGTGGCGATCGGGGCTCCCGCT	2449
Oy		765	lThIleUTrIllePheTyAsPthrCIyTYrThrgIuarTyrmEtGLYNhsProAspI	785
D	b	2450	CACCGTGTGATGGCTTACACACACAGGTAACACTGACGCTCAATGAGACGTCCCGAADA	2509
Oy		785	pAsnGLuIGLYTyTyTLyeuGLySerAlAlamEtGlAlaGLuLySpheProSerGI	805
D	b	2510	CAACACACAGGCTATGAGGCGGGTTCCTGGCCCTGCACGTGGAGAAAGCTGCCAACGA	2569
Oy		805	uProAsnArGLeuLeuLeuHIsGLyPheLuAspLIuAsnaVlnIsPheAlAnIsTh	825
D	b	2570	GCCCAACCGCTTCTATCTCCACACGCGTTCCTGGACGAAACGTGCACATTTCACAC	2629
Oy		825	rSerIlleuLeuSerPheLuValrGLuLySProTyraSpleu-----	841
D	b	2630	AAATCTCTGTCTCCAACTGATCCGACAGGAAACCTTACACGTCACAGTGGCCCT	2689
Oy		842	-----GlnIleTyProGLuGLuarGHisSerIleArGValProGLuSe	856
D	b	2690	GCTCTCTGTCTCCCGCAGATCTACCCCAAGAGAGACACATATTCCTGCCCGGACCT	2749
Oy		856	rGLyGLuHIsTyrgIuLeuHIsLeuLeuHIsTyrlEuGLInGLuAsnLeu	872
D	b	2750	GGGGAGACACTAAGAATGACAGTTCCTGCACATTTCACAGAAATCTCTC	2798
RESULT 28				
ABK83341				
ID	ABK83341	standard;	CDNA; 4037 BP.	
XX	ABK83341:			
AC				
XX				
DT	12-AUG-2002	(first entry)		
DE				
XX	cDNA encoding human DPRP-2 splice variant #9.			
KW	Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;			
KW	DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;			
KW	diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;			
KW	heart failure; hypertension; urinary retention; osteoporosis; cancer;			
KW	ulcer; allergy; cancer; psychotic disorder; neurological disorder;			
KW	dyskinesia; reproductive disorder; inflammatory disorder;			
KW	metabolic disorder; gene; ss.			
OS	Homo sapiens.			
PN	MO2002J1134-A2.			
XX				
PD	18-Apr-2002.			
PF	12-OCT-2001, 2001WO-US31874.			

PR	12-OCT-2000; 2000US-240117P.		
PA	(FERR) FERRING BV.		
PI	Q1 S, Akinsanya KO, Riviere PJ, Junien J;		
DR	WPI: 2002-444178/47.		
XX	P-PsDB; ABC61610.		
PT	New dipeptidyl peptidase IV-related proteins and nucleic acids encoding		
PR	the proteins, useful for treating e.g. fungal, bacterial, protozoan and		
PT	viral infections, cancers, allergies, neurological disorders, or pain		
PS	-		
PS	Disclosure; Page 103-104; 113pp; English.		
CC	The present invention relates to the isolation of novel human serine		
CC	proteases referred to as dipeptidyl peptidase IV (DPPIV)-related		
CC	proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)		
CC	and nucleic acids encoding them are useful for treating infections		
CC	such as fungal, bacterial, protozoan and viral infections, particularly		
CC	infections caused by human immunodeficiency virus (HIV-1 or HIV-2),		
CC	pain, diabetes, precocious puberty, infertility, obesity, anorexia,		
CC	bulimia, Parkinson's disease, acute heart failure, hypotension,		
CC	hypertension, urinary retention, osteoporosis, angina pectoris,		
CC	stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,		
CC	psychotic and neurological disorders (e.g. anxiety, dementia, or		
CC	schizophrenia), and dyskinestias. These may also be used in discovering		
CC	therapeutic agents for the treatment of reproductive, inflammatory and		
CC	metabolic disorders. ABK83322-ABK83343 encode human DPPR proteins.		
XX			
SQ	Sequence 4037 BP; 869 A; 1268 C; 1131 G; 769 T; 0 other:		
Alignment Scores:			
Pred. No.:	3,86e-255	Length:	4037
Score:	2599.50	Matches:	479
Percent Similarity:	71.82%	Conservative:	125
Best Local Similarity:	56.96%	Mismatches:	173
Query Match:	55.31%	Indels:	64
DB:	24	Gaps:	4
US-10-070-464-1 (1-882) x ABK83341 (1-4037)			
OY	35 PheTYrValGluArgTYrSerTrpSerGlnLeuLYsLysLeuAlaAspThrArgLYs 54		
DB	436 TTCAGAGCGTCACAGAAGACACTCGTGGGAGCGGTCCGGAGCATCATCCAGCGAGCCGCAAG 495		
OY	55 TYrHisGLYTYrMetEcALALySaLaPaROHIsAspPhMeTcHeVaLLySaRgnaSP 74		
DB	486 TACTCGGCGCTCATTTGTCAACAAGCGGCCCGCCAGCACTTCACATTGTCTGCAGAAAGCAGAT 555		
OY	75 ProASpGLYProOHISerSraSPArGIleTYrTYrLeuAlaMeTserGLYLusAnRGlu 94		
DB	556 GAGTCTGGGCCCCACACTCCACC GCCCTCTACTGATCTCGGATCCATATGCAAGCCAGAG 615		
OY	95 AsnThrLeuPheTYrSerGIuIleProlYSThrILeasNARGaLaAlaValLeuMcLeu 114		
DB	616 AACCTCCCTCTACTACTCTGAGATTTCCCAAGAAAGTGCCGAAGAGSGCTTGCTGCTCG 675		
OY	115 SerTRPLYSProLeuLeuAspLeuPheGlnAlaThrLeuAspTRYrGLYMeTYrSerArg 134		
DB	676 TCCTGGAGACATGCTGTGATCTTCCAGGCGCACCCGCCACCATGAGGGGTCTACTCTCG 735		
OY	135 GluInUGluLeuLeuARGLuArgLYsArgILeGIlyThValGLYILeAlaSerTYrAsp 154		
DB	736 GAGGAGGAGCTCTGAGGAGCGGAACCCCTGGGGGCTTCCGGCATACCTCTTAACGAC 795		
OY	155 TYrHisGLNGLySerGLYThrPheLeuPheGlnAlaGLYSerGLYILeTYrHisValLYs 174		
DB	796 TTCCACAGGAGAGAGGGCTTTCTCTTCCATTCAGAGCGACAGAACAGGCTCTTCCACATGCGCG 855		
OY	175 AspGLYGLYProGLNGLyPheThrChlNGlinProLeuLeuArgProAsnLeuValGlUThrSer 194		

Dd	856	GAGCGCGCAAGAACGGCTTCATGAGTGTCCCTATGAACCGGTGGAATCAAGCCAG	915
Oy	135	CysProAsnIleAqMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe	214
Dd	916	TGCTCAGGCGCCCGAATGGAGCCCAAAATTTGGCCCTGGCCAGCCCTGCTTCTCCCTTC	975
Oy	215	IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr	234
Dd	976	ATCATATACACCGACCTGTGGTGCCCACTGAACTGAACAGCAGGACGGCGCTGACC	1035
Oy	235	TyrValHisAsnGluLeuAlaAsnMetGluAspAlaArgSerAlaGlyValAlaThr	254
Dd	1036	TTTCGCCACCAAGGTTATTCATATGTCCTGGATGAGCCCAAGCTGGCGGTGGCCACC	1095
Oy	255	PheValLeuGlnGluGluIlePheAspArgTrpSerGlyTyrTrpTrpCysProLysAla	274
Dd	1096	TTTCGTATACAGGAAGAGTTTCAGCCGCTTACTGGGTACTGGGGGCCCCACACCTCC	1155
Oy	275	ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspLeuSer	293
Dd	1156	TGGGAGGTTGACAGGGCCCTCAAGACGCTCGAATCTGTATAGAGAACTGATGATGCC	1215
Oy	294	GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaSerPhe	313
Dd	1216	GAGGAGGAGCATTCACGCTCCCTCCGCTGAGAAAGAAAGAGCAGCATCGAT	1275
Oy	314	ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet	333
Dd	1276	CGGTACCCCAAGACAGCAGCAGCAAGAAATCCCAAGATTGCCTTGAACTGGCTGATTCAG	1335
Oy	334	IleAspAlaGluGluArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu	353
Dd	1336	ACTGACACCCAGGGCAAGATCTGCTGCACCAAGAAAGAGAGCTGGTGGAGCCCTTTCAGC	1395
Oy	354	IleLeuPheGluGluValGluTyrIleAlaArgAlaGluTyrThrProGluGluLysTyr	373
Dd	1396	TGCCTGTTCCCGAGAGTGGAGTACATGCCAGGGCGGGTGGACCCGGATGCAAAATAC	1455
Oy	374	AlaTrpSerIleLeuLeuAsnAspArgSerGlnThrArgLeuGlnIleValIleLeuSerPro	393
Dd	1456	GCTCGGGCCATGTTCCCTGGAGACGGGCCACAGACATGGCTCCAGCTCCTCCTCCGCCCG	1515
Oy	394	GluLeuPheIleProValGluAspAspValMetGluArgGluArgLeuIleGluSerVal	413
Dd	1516	GCCTGTTCACTCCCGAGACACAGAAATGAAGAGCAGCGCTAGCTCTCCAGACGTCTC	1575
Oy	414	ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle	433
Dd	1576	CCCAGAGATCCAGCGCGTATGGTGTTACAGAGAGTCAACCACTGTCATCAATGTT	1635
Oy	434	HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe	452
Dd	1636	CATGACATCTTATATCCCTTCCCAATCAAGAGAGAGACAGCATGCTTCTTCCGC	1695
Oy	453	AlaSerGluCysLysThrGlyPheArgHisIleTyrLysIleIleThrSerIleLeuLysGlu	472
Dd	1696	GCCATGATGATCAAGACCGGCTGTGCATTTGTACAAAGTCAACGCGCTTTAAATCC	1755
Oy	473	SerLysTyrLysAspSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle	492
Dd	1756	CAGGCGTACGATGGATGAGCCCTTCAGCCCGGGAAGATGAATTTAAGTCCCTCATTT	1815
Oy	493	LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGluValArgHisGlySerAsn	512
Dd	1816	AAGCAAGATGCTCTGACACAGCGGTGAATGGAGATTTTGGCGAGCACGGCTCC---	1872
Oy	513	IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu	532
Dd	1873	-----AAGGGACCAAGACACGCGCGTG	1896
Oy	533	GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp	552
Dd	1897	GAGACACACCTTACAGTGCTACCTATGAGCGCGCGGGAAGTCTGACGCTCAACCG	1956

QY	553	ArgIglYrSerHnSsrCYsLysISeSgLnHsCYsAsPhePhLlSerLysTyr	572
Db	1957	CCCGGCTTTCCTCCATACCTGCTCCATGAGCCAGAACCTTGACATGTGCTGATACGCCTAC	2016
QY	573	SerAnSgLnYsAsnProHnSsCYsValSerLeuTyrLysLeuSerSerProGlnuAsp	592
Db	2017	AGCAGCGnAGACACGCGCCCTCGnTGCACGnCTCAACACTGAGCGGCGCCGACGAGCAC	2076
QY	593	ProHnCYsLysThrLysGlnPheThrPalnThrLleLeuAspSerAlaGlyProLeuPro	612
Db	2077	CCCGTCGACAAAGCACGCCCTCTCGGGTAGAGnTnGAGGACGACGCTGCCCGCCG	2136
QY	613	AspYrThrProProGlnLlPheSerPheGluSerThrThGlyPheThrLeuTyrGly	632
Db	2137	GATTATGTCTCTCCAGAGATCTTCATTTCCACAGCGCTGGAGnTGCCTACGCGC	2196
QY	633	MetLeuTyrLysProHnSsAsPheGlnProGlyLysLysTyrProThrValLeuPheLle	652
Db	2197	ATGATCTTACAAAGCCCCACGCGCTTGACGACGAGAGAAACACCCACGCTCTGTTGTA	2256
QY	653	TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg	672
Db	2257	TATGAGAGCCCCCAGGCGAGCTGnGATATACCTCTCAAGGATCAACTACTTGCGG	2316
QY	673	LeuAsnThrLeuAlaSerLeuGlyTyrValValValValAlaAspAsnArgGlySerCYs	692
Db	2317	CTCAACACACTGCGCTCCGAGGGCTACGCGCTGCTGATTTAGACGAGCGGCGCTCGT	2376
QY	693	HnSArgGlyLeuLysPheGlnGlyAlaPheLysTyrLysMetGlyGlnLleGlnLLeAsp	712
Db	2377	CAGCGAGGCGTTCGGTTTCGAAGGGCGCCCTGAAAAACCAATATGGCCAGCTGAGATCAG	2436
QY	713	AspGlnValGlnGlyLeuGlnTyrLeuAlaSerArgTyrAspPheLlAspLeuAspArg	732
Db	2437	GACCAAGGGGAGGGCTGCGAGTTCTGnGCCAGACAGATAGGCTTATGAGCTTGACCGCA	2496
QY	733	ValGlyLlHnSgLYrPserTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg	752
Db	2497	GnTGCGATCCATGCGCTGCTCTAGAGGGCGCTCTGCTCATGAGGGCTATATCCACAG	2556
QY	753	SerAspLlePheArgValAlaLleAlaGlyAlaProValThrLeuThrLlPheTyrAs	772
Db	2557	CCCCAGGCTTCAAG-----	2572
QY	772	PThnGlyTyrThrGlnArgTyrMetGlnHnSProAspGlnAsnGlnGlnGlyTyrGlye	792
Db	2572	-----	2572
QY	792	uGlySerValAlaMetGlnAlaGlnLysPheProSerGlnProAsnArgLeuLeuLe	812
Db	2573	-----CCCAACGCGTTCATTACT	2592
QY	812	uHnSgLYrPheLeuAspGlnuAsnValHnSphnAlaHnSThrSerLlLeuLeuSerPheLe	832
Db	2593	CCAGCGGCTCTCTGACCAAAACGTGCACTTTTCCACAAACTTCGnTCTCCACT	2652
QY	832	uValArgAlaGlyLysProTyrAsPheGlnGlnLlTyrTyrProGlnGlnuArgHnSerLleAr	852
Db	2653	GATCCGAGACAGGAAACTTACCAAGCTCCAGATCTACCCCAACGAGAGACACAGATTTCG	2712
QY	852	gValProGlnSerGlyGlnHnSgLYrGlnuHnSLeuHnSLeuHnSgLYrLeuGlnGlnuAsnLe	872
Db	2713	CTGCGCCGAGTGGGAGACATnTGAAGTACAGCTTGCTGCACTTTCACAGGAATACT	2772
QY	872	u 872	
Db	2773	C 2773	
RESULT 29			
ID	ABR83340	standard; cDNA; 4120 BP.	
XX			

AC ABRK3340:
 XX 12-AUG-2002 (first entry)
 XX
 DE cDNA encoding human DPRP-2 splice variant #8.
 XX
 KW Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder; gene; ss.
 XX
 XX Homo sapiens.
 OS
 PN MO200231134-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US31874.
 XX
 PR 12-OCT-2000; 2000US-240117P.
 XX
 PA (FERR) FERRING BV.
 PI Q1 S, Akinsanya KO, Riviere PJ, Junien J;
 XX
 DR WPI: 2002-444178/47.
 XX P-PSDB: ABRK3340.
 PS
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 XX
 XX
 XX Disclosure; Page 100-101; 113pp: English.
 XX
 XX The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABRK3342-ABRK3343 encode human DPRP proteins.
 XX
 SO Sequence 4120 BP; 884 A; 1298 C; 1162 G; 776 T; 0 other:
 Alignment Scores:
 Pired. No.: 3,98e-255 Length: 4120
 Score: 2599.50 Matches: 479
 Percent Similarity: 71.82% Conservative: 125
 Best Local Similarity: 56.96 Mismatches: 173
 Query Match: 55.318 Indels: 64
 DB: 24 Gaps: 4
 US-10-070-464-1 (1-882) x ABRK3340 (1-4120)
 QY 35 PheTyrValAlaGlnArgTyrSerTrpSerGlnLeuLeuLysLeuLeuAlaAspThrArgLys 54
 DB 436 TTCACGTCGACGAGACGTCGTGGGACGGGCTCCGAGCATCTCCACGCGCCGACG 495
 QY 55 TYTHISGLTYTymetmetalaLysAlaProHisAspPheMetPheValLysATGAsnASP 74
 DB 496 TACGTGGGCTGCTATTGTCAACAAGGGCCGACGACTTCCAGTTTGTGCAAGAAGCGGAT 555

QY 75 ProAspGlyProHisSerAspArgLysTyrTyrLeuAlaMetSerGlyLysAsnArgLys 94
 DB 556 GAGTCGTGGGCCCCACCTCCACCGCTCTACTACTCGGATGCCATATGACCGCCAGAG 615
 QY 95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaValAlaLeuMetLeu 114
 DB 616 AACCTCCCTCTACCTGATCTGAGATTCCCAAGAGTCCGGAAGAGCTCTGCTGCTCTG 675
 QY 115 SerThrLysProLeuLeuAspLeuPheGlnAlaThrLeuAspPyrGlyMetTyrSerArg 134
 DB 676 TCTCGAAGACGATGCTGATCTTTCACAGCCACGCCACCATGGGCTCTCTCGG 735
 QY 135 GluGluGluLeuLeuArgLysArgLysArgLysArgLysArgLysArgLysArgLys 154
 DB 736 GAGGAGAGAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 795
 QY 155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaLysSerGlyLysArgLysVal 174
 DB 796 TTCACAGCGAGAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
 QY 175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
 DB 856 GACGGCGGACAGAACGCTTCATGCTGCTCCCTATGAAACCGCTGGAATCAAGACCCAG 915
 QY 195 CysProAsnIleArgMetAspProLysLeuGlyProAlaAspProAspThrIleAlaPhe 214
 DB 916 TGCTCAGCGCCCGGATGAGACCCCAAAATGCTGCGCCTGCGCCTGCTCTCTCTCT 975
 QY 215 IleHisSerAsnAspIleThrPheSerAsnIleValThrArgGluGluArgLysThr 234
 DB 976 ATCAATTAACAGCAGCAGCTGTGGTGGCCACATCAGACAGCAGCAGCAGCAGCAGC 1035
 QY 235 TYTValHisGlnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
 DB 1036 TTCTGCACCAAGACTTATTCATATGCTGATGATGATGATGATGATGATGATGATG 1095
 QY 255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
 DB 1096 TTCGTATACAGAGAAGATTGCGACCGCTTACATGAGTGGTGGTGGTGGTGGTGGT 1155
 QY 275 ThrThrProSerGlyGlyLysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
 DB 1156 TGGGAAGCTTCAAGAGGCTCAAGAGCCTGCAATCTGTATGAGGAAGTCGATGATGCC 1215
 QY 294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
 DB 1216 GAGGTGAGGTCTATTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1275
 QY 314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
 DB 1276 CGGTACCCCGAGCAGGACGACCAAGAAATCCCAAGATTGCTTGAACATGCTGAGTTCCAG 1335
 QY 334 IleAspAlaGluGlyArgLysIleLeuAspValIleAspLysGluLeuIleGlnProPheGlu 353
 DB 1336 ACTGACAGCGCAGGCAAGATGCTGACCCAGCAGCAAGAGAGCTGGTGCAGCTTCAGC 1395
 QY 354 IleLeuPheGluGluValGluTyrTyrIleAlaArgAlaGlyThrPheProGluGlyLys 373
 DB 1396 TCGCTGTTCGCAAGGTGAGGATGATGCGCAGGCGCGGAGGAGGAGGAGGAGGAGGAG 1455
 QY 374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
 DB 1456 GCGTGGGCGCATGTTCCGAGGAGCGGCGCCACAGTGGCTTCAGCTGCTGCTGCTGCT 1515
 QY 394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
 DB 1516 GCCCTGTTCATCCGAGCAGACAGAAATGAGAGCAGCAGCGCTTACCTTCAGAGCTGTC 1575
 QY 414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleThrIleAsnIle 433
 DB 1576 CCGAGGAATTCAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1635
 QY 434 HisAspIlePheHisValPheProGlnSerHisGluGluGluIleGluPheIlePhe 452

[illegible][illegible]

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression.
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, Leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX
SQ Sequence 3262 BP; 687 A; 1019 C; 931 G; 625 T; 0 other:

Alignment Scores:

Pred. No.:	1,09e-242	Length:	3262
Score:	2476.50	Matches:	462
Percent Similarity:	74.12%	Conservative:	125
Best Local Similarity:	58.33%	Mismatches:	166
Query Match:	52.69%	Indels:	40
DB:	22	Gaps:	6

US-10-070-464-1 (1-882) x AA157880 (1-3262)

QY 92 AsnArgGlnAsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaIleVal 111
DB 41 AGCGGAGAGAACTCCCTCTACTGTGAGATTCATT -CAAGTCGCGAAGAGGCTCTG 99
QY 112 LeuMetLeuSerTrpLysProLeuLeuAspLeuPheGlnIleThrLeuAspTyrGlyMet 131
DB 100 CTGCTCTGCTCTGGAAGCAGATGCTGATCATTTCCAGGCGACGCCCAACCATGGGCTC 159
QY 132 TyrSerArgGluGluLeuLeuLeuArgGluArgLysArgIleGlyThrValIleAla 151
DB 160 TACTCTGGGAGGAGGAGGAGCTGTGAGGAGCGAAGCCCTGGGGCTTCGGCATACC 219
QY 160 TACTCTGGGAGGAGGAGGAGCTGTGAGGAGCGAAGCCCTGGGGCTTCGGCATACC 219
QY 152 SerTyrAspTyrHisGlnGlySerGlyThrPheLeuPheGlnIleGlySerGlyIleTyr 171
DB 220 TCTTACACACTTCCACAGCGAGTGGCTCTCTCTTCCAGGCGCACACAGCCTTTC 279
QY 172 HisValLysAspGlyGlyProGlnGlyPheThrGlnIleProLeuAspProAsnLeuVal 191
DB 280 CGCTGGCGGAGGAGGAGGAGGAGGCTTATGCTGCTCCCTATGAAACGCGTGGAAATC 339
QY 192 GluThrSerCysProAsnIleArgMetAspProLysLeuGlyProAlaAspProAspTyr 211
DB 340 AAGACCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399
QY 212 IleAlaPheIleHisSerAsnAspIleTrpIleSerAsnIleValIleThrArgGluArg 231
DB 400 TTCCTCTCATATACATACAGCAGCTGTGGTGGCCAAATCCGAGACGAGGAGGAGGAG 459
QY 232 ArgLeuThrTyrValHisAsnGluLeuAlaAsnMetGluLeuAspAlaArgSerAlaGly 251
DB 460 CGGCTGACCTTCTGCCCAAGAGTTTATCCAAATGCTCTGGATGACCCCAAGTGTGCGGT 519
QY 252 ValAlaThrPheValLeuGlnGluLeuPheAspArgTyrSerGlyTyrTrpCysPro 271
DB 520 GTGGCCACCTTGTGATACAGAGAGTTCGACCGCTTCACTGGGTACTGTGTGCGCC 579
QY 272 LysAlaGluThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGlnAsn 290
DB 580 ACAACCTCCCTGGGAAGGTTGAGAGGCTTCAAGACGCTGGCAATCTGTATGAGAGATC 639
QY 291 AspGluSerGluValGluIleIleHisValThrSerProMetLeuGluThrArgAla 310
DB 640 GATGAGTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699
QY 311 AspSerPheArgTyrProLysThrGlyThrAlaAsnProLysValIleThrPheLysMetSer 330
DB 700 GACTCGATCGGATACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 759
QY 331 GluIleMetIleAspAlaGluArgIleIleLeuAspValIleAspLysGluLeuIleGln 350
DB 760 GAGTTCAGACTGACAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 819

QY 351 ProPheGluIleLeuPheGluGluValGluTyrIleAlaArgAlaGlyTrpThrProGlu 370
DB 820 CCTTACAGCTCGCTGTTCCGAGAGGTGAGTACTCCGAGGCGGGGTGAGCCGGGAT 879
QY 371 GlyLysTyrAlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeu 390
DB 880 GGCAATATACCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 939
QY 391 IleSerProGluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIle 410
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QY 411 GluSerValProAspSerValIleProLeuIleIleTyrGluGluThrThrAspIleTrp 430
DB 1000 AGAGCTGTCCCGACAGATGTCACCGCCTATGCTGTGAGGAGGAGGAGGAGGAGGAGGAG 1059
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QY 550 LeuThrAspArgGlyTyrSerHisSerCysLysIleSerGlnHisCysAspPhePheIle 569
DB 1363 CTCACACAGCGCGGCTTCTCCATAGCTGTCATGAGCCAGACCTTCGACATTTGCTGC 1422
QY 570 SerLysTyrSerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerPro 589
DB 1423 AGCCACTACAGCAGCAGTGCAGCAGCCCGCTGTCAGCTTCAAGCTGAGCGGCGCC 1482
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DB 1483 GACACAGACCCCTGACAGACAGCCCGCTTCTGGCTGACATGATGAGGAGGCC--- 1539
QY 610 ProLeuProAspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThr 629
DB 1540 -----AAGATCTTTCATTTCCACAGCGGCTGCGAGTGC 1575
QY 630 LeuTyrIleMetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrVal 649
DB 1576 CTCTACGCGATGATCTACAGCCCGCAGCAGCTTGCAGCAGGAGGAGGAGGAGGAGGAG 1635
QY 650 PhePheIleTyrGlyGlyProGluValGluIleValAsnAsnArgPheLysGlyValAsn 669
DB 1636 CTCTTTTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1695
QY 670 TyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArg 689
DB 1696 TACTTGGGCGTCAACACACTGCGCTCCCTGGGCTAGCCGCGTGTGATGAGGAGGAGGAG 1755
QY 690 GlySerCysHisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIle 709
DB 1756 GGCTCTCTGTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1815

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OY 710 GluIleAspArgGlnValGluGlyLeuGlnIleuAlaSerArgTyrAspPheIleAsp 729
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Db 1816 GAGATCGAGGACACAGGTGGAGGGCTGCATGCTGGCCGAGAAATAGCCTCATCGAC 1875
OY 730 LeuAspArgValGlyIleHisGlyTyrSerTyrGlyGlyTyrLeuSerLeuMetAlaLeu 749
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Db 1876 CTGAGCCGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1935
OY 750 MetGlnArgSerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIle 769
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Db 1936 ATCCACAAGCCCAAGGCTGTCAGAGTGGCCATCCGGGCTGCCCGCTCACCGTGGATG 1995
OY 770 PheTyrAspIleGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGly 789
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Db 1996 GCCTACGACACAGGGGTACACTGACGCTACATGACGCTCCTGAGAACACACAGCAGCGC 2055
OY 790 TyrTyrLeuGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeu 809
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OY 810 LeuLeuLeuHisGlyPheLeuAspGlnAsnValHisPheAlaHisThrSerIleLeuLeu 829
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Db 2236 CCGAGAGATCTACCCCAACGAGAGACACAGTATTCGCTGCCCCGAGTCCGGGAGACACTAT 2295
OY 861 GluLeuHisLeuLeuHisTyrLeuGlnIleAsnLeu 872
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Db 2296 GAAGTCAAGCTGTGCTGCTTCTTACAGGAAATACCTC 2331
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Search completed: May 19, 2003, 15:54:36
Job time : 7841 secs

PR 18-FEB-2000; 2000AU-0005709.
 XX
 XX (UNSY) UNIV SYDNEY.
 XX
 PI Abbott CA, Gorell MD;
 XX
 XX WPI; 2001-281520/29.
 DR N-PSDB; AAC85694.
 XX
 PT New human dipeptidyl aminopeptidase (DPP8) useful for cleaving
 PT substrates, identifying inhibitors of DPP8 catalytic activity which
 PT have therapeutic uses, and for detecting activated T cells
 XX
 XX Claim 1; Fig 2; 78pp; English.
 CC This sequence represents human dipeptidyl aminopeptidase (DPP8).
 CC DPP8 has substrate specificity for H-Ala-Pro-PNA, H-Gly-Pro-PNA and
 CC H-Arg-Pro-PNA. Therefore, it is a prolyl oligopeptidase and a
 CC dipeptidyl peptidase, because it is capable of hydrolysing the
 CC peptide bond C-terminal to Pro in each of these compounds. DPP8
 CC is homologous with human DPPiv. DPP8 is useful for cleaving a
 CC substrate, and for detecting an activated T cell which involves
 CC measuring the level of DPP8 gene expression in a T cell. The level
 CC of DPP8 expression is detected by detecting the amount of DPP8 RNA
 CC in the cell. It is also useful for identifying a molecule capable
 CC of inhibiting the cleavage of the substrate by DPP8. Molecules
 CC identified as inhibiting DPP8 catalytic activity may be useful for
 CC treating diarrhoea, growth hormone deficiency, lowering glucose levels
 CC in non-insulin dependent diabetes mellitus and other disorders
 CC involving glucose intolerance, enhancing mucosal regeneration and
 CC as immunosuppressants.
 CC
 XX
 XX
 SQ Sequence 882 AA;
 Query Match 100.0%; Score 4700; DB 22; Length 882;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAMETEOLEVEIFETADCEENIESODRPLEPFYERYYSWSOLKLLADTRKHGMM 60
 1 MAAMETEOLEVEIFETADCEENIESODRPLEPFYERYYSWSOLKLLADTRKHGMM 60
 DB 1 MAAMETEOLEVEIFETADCEENIESODRPLEPFYERYYSWSOLKLLADTRKHGMM 60
 QY 61 AKAPHEMFYKRNPDGPHSDRIYLLAMSGENRENTLFYSEIPTINRAVLMISMPRL 120
 61 AKAPHEMFYKRNPDGPHSDRIYLLAMSGENRENTLFYSEIPTINRAVLMISMPRL 120
 DB 61 AKAPHEMFYKRNPDGPHSDRIYLLAMSGENRENTLFYSEIPTINRAVLMISMPRL 120
 QY 121 DLFOATLDYGYRSREBELLRKRRTIGVIGASYDYGSGFELFOAGSGIYHVDGPGOG 180
 121 DLFOATLDYGYRSREBELLRKRRTIGVIGASYDYGSGFELFOAGSGIYHVDGPGOG 180
 DB 121 DLFOATLDYGYRSREBELLRKRRTIGVIGASYDYGSGFELFOAGSGIYHVDGPGOG 180
 QY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSDNIWISNIVTREERLTYVHNE 240
 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSDNIWISNIVTREERLTYVHNE 240
 DB 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSDNIWISNIVTREERLTYVHNE 240
 QY 241 ANMEEDARSAGVATFYQEEEDRISGYWCCKAETTPSGKILRLIYENDESEVEIIVH 300
 241 ANMEEDARSAGVATFYQEEEDRISGYWCCKAETTPSGKILRLIYENDESEVEIIVH 300
 DB 241 ANMEEDARSAGVATFYQEEEDRISGYWCCKAETTPSGKILRLIYENDESEVEIIVH 300
 QY 301 TSPLETRRADSFYRPTGTANPKVTFKMSFIMIDAGRILIDVIDKELIOFEILLFSGVE 360
 301 TSPLETRRADSFYRPTGTANPKVTFKMSFIMIDAGRILIDVIDKELIOFEILLFSGVE 360
 DB 301 TSPLETRRADSFYRPTGTANPKVTFKMSFIMIDAGRILIDVIDKELIOFEILLFSGVE 360
 QY 361 YIARAGWTEGKYAMSLILDRSOTRLQIVLISPELFIPEVDVVEROLLESVPDSVPL 420
 361 YIARAGWTEGKYAMSLILDRSOTRLQIVLISPELFIPEVDVVEROLLESVPDSVPL 420
 DB 361 YIARAGWTEGKYAMSLILDRSOTRLQIVLISPELFIPEVDVVEROLLESVPDSVPL 420
 QY 421 IYIETTDIWNIDITHVPPQSHHEEIEFTFASECKTGFFHLKITSILKESYKNSG 480
 421 IYIETTDIWNIDITHVPPQSHHEEIEFTFASECKTGFFHLKITSILKESYKNSG 480
 DB 421 IYIETTDIWNIDITHVPPQSHHEEIEFTFASECKTGFFHLKITSILKESYKNSG 480
 QY 481 GLPAPSDFKCPKEIKELITSGEMEVLRHGSNIQVDEVRRIYVEEGKDSPLEHLLVVS 540
 481 GLPAPSDFKCPKEIKELITSGEMEVLRHGSNIQVDEVRRIYVEEGKDSPLEHLLVVS 540
 DB 481 GLPAPSDFKCPKEIKELITSGEMEVLRHGSNIQVDEVRRIYVEEGKDSPLEHLLVVS 540

QY 541 YVNGEYTRLDRCYSHSCISQHCDFEISKYSNOKNPHCVSLYKLSPPDDPTCKTEF 600
 541 YVNGEYTRLDRCYSHSCISQHCDFEISKYSNOKNPHCVSLYKLSPPDDPTCKTEF 600
 DB 541 YVNGEYTRLDRCYSHSCISQHCDFEISKYSNOKNPHCVSLYKLSPPDDPTCKTEF 600
 QY 601 WATILDSAGPLPDYTPPEIFSESTGTLYGMLKPHDLQPKKPYVLEFYGGPOVL 660
 601 WATILDSAGPLPDYTPPEIFSESTGTLYGMLKPHDLQPKKPYVLEFYGGPOVL 660
 DB 601 WATILDSAGPLPDYTPPEIFSESTGTLYGMLKPHDLQPKKPYVLEFYGGPOVL 660
 QY 661 VNNFKGVKFRNLTLASLSGVVYVINDRSGCHNGKLFEGAFKMKQIETDOVELOY 720
 661 VNNFKGVKFRNLTLASLSGVVYVINDRSGCHNGKLFEGAFKMKQIETDOVELOY 720
 DB 661 VNNFKGVKFRNLTLASLSGVVYVINDRSGCHNGKLFEGAFKMKQIETDOVELOY 720
 QY 721 LASRYDEIDLDKRVGSHGMSYGYLSLMAQLMQRSDIFRVAIAGAPVTLMIFDYGTERYM 780
 721 LASRYDEIDLDKRVGSHGMSYGYLSLMAQLMQRSDIFRVAIAGAPVTLMIFDYGTERYM 780
 DB 721 LASRYDEIDLDKRVGSHGMSYGYLSLMAQLMQRSDIFRVAIAGAPVTLMIFDYGTERYM 780
 QY 781 GHDPQNEGYLLGSVAMQAEKFPSEPNRLLLHGFIDENVHFAHTSTILSFLVRAGKPYD 840
 781 GHDPQNEGYLLGSVAMQAEKFPSEPNRLLLHGFIDENVHFAHTSTILSFLVRAGKPYD 840
 DB 781 GHDPQNEGYLLGSVAMQAEKFPSEPNRLLLHGFIDENVHFAHTSTILSFLVRAGKPYD 840
 QY 841 LQIYPOERHSTRPESEGEHELHLHYLOENLGSRIALKVI 882
 841 LQIYPOERHSTRPESEGEHELHLHYLOENLGSRIALKVI 882
 DB 841 LQIYPOERHSTRPESEGEHELHLHYLOENLGSRIALKVI 882
 RESULT 2
 AAE24170
 ID AAE24170 standard; Protein; 882 AA.
 XX
 AC AAE24170;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human dipeptidyl peptidase 8 (DPP8) protein.
 XX
 KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
 KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
 KW graft rejection; anti-diabetic; anti-inflammatory; immunosuppressive;
 KW antiviral; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200234900-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001MO-AU01388.
 XX
 PR 27-OCT-2000; 2000AU-0001078.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Abbott CA, Gorell MD;
 XX
 XX WPI; 2002-454646/48.
 DR N-PSDB; AAD38956.
 XX
 PT New dipeptidyl peptidase (DPP) peptides, useful for screening
 PT inhibitors of DPP catalytic activity, which may be employed to treat
 PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
 PT rejection and HIV infection -
 XX
 PS Example; Fig 1; 91pp; English.
 XX
 CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
 CC polynucleotides encoding such proteins. The DPP peptides are useful for
 CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
 CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
 CC rejection and HIV (human immuno deficiency virus) infection. The present
 CC sequence is human DPP8 protein.
 XX
 SQ Sequence 882 AA;

Query Match	100.0%;	Score 4700;	DB 23;	Length 882;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 882;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAAMETBOLGVIFETADCEENIESODRPKLEPFYVERYSMSQLKLLADTRKRYGYM	60	
DB	1	MAAMETBOLGVIFETADCEENIESODRPKLEPFYVERYSMSQLKLLADTRKRYGYM	60	
QY	61	AKAPHFMEVKRRNDPGPHSDRIYYLAMSGENRENTLFYSEIKPTINRAVLMLSKPLL	120	
DB	61	AKAPHFMEVKRRNDPGPHSDRIYYLAMSGENRENTLFYSEIKPTINRAVLMLSKPLL	120	
QY	121	DLFOATLDYGMTSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG	180	
DB	121	DLFOATLDYGMTSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG	180	
QY	181	FTQOPLRPNLVEISCPNIRMDPKLCPADPDMIAFIHNDIWNISNIYTRERRLTYVHNEL	240	
DB	181	FTQOPLRPNLVEISCPNIRMDPKLCPADPDMIAFIHNDIWNISNIYTRERRLTYVHNEL	240	
QY	241	ANNEEDARSAGVATFVLOEEFDRTSGYWMCPKATTPSGGKILRLIYEENDESEVEIHY	300	
DB	241	ANNEEDARSAGVATFVLOEEFDRTSGYWMCPKATTPSGGKILRLIYEENDESEVEIHY	300	
QY	301	TSPMLETRRADSFRRYKGTGTANKVTFKMSIEMIDAGRIIDVDEKELIPEILEGVE	360	
DB	301	TSPMLETRRADSFRRYKGTGTANKVTFKMSIEMIDAGRIIDVDEKELIPEILEGVE	360	
QY	361	YIARAGMTPEGKYAMSILLDRSOTRQIYLISPELFIYEDDVMERORLIESVPSVTPL	420	
DB	361	YIARAGMTPEGKYAMSILLDRSOTRQIYLISPELFIYEDDVMERORLIESVPSVTPL	420	
QY	421	IIEETTDIWINHDIHFVPOSHHEIEFIETFAECKTGRIHLYKTSTLKEKYSRSSG	480	
DB	421	IIEETTDIWINHDIHFVPOSHHEIEFIETFAECKTGRIHLYKTSTLKEKYSRSSG	480	
QY	481	GLPAPSDFCPIKEEIAITSGEMEVLRHGSNIQVDEVRLVYFECTKDSPLEHNLVVS	540	
DB	481	GLPAPSDFCPIKEEIAITSGEMEVLRHGSNIQVDEVRLVYFECTKDSPLEHNLVVS	540	
QY	541	YVNRGEVTLTDGYSHSCCISCHCFEISKYSNOKNPHCVSLKXISPPDDPTCKTER	600	
DB	541	YVNRGEVTLTDGYSHSCCISCHCFEISKYSNOKNPHCVSLKXISPPDDPTCKTER	600	
QY	601	WATILDSAGRLPYTPPELTFSESTTGFTLYGMLYKPHDQPEKKTPLYLETIGGQVOL	660	
DB	601	WATILDSAGRLPYTPPELTFSESTTGFTLYGMLYKPHDQPEKKTPLYLETIGGQVOL	660	
QY	661	VNRRFGVYKFRNLTLASLGYYVVVIDNRSCHRGKLFEGAFKRYKMGQIEIDQVEGLQY	720	
DB	661	VNRRFGVYKFRNLTLASLGYYVVVIDNRSCHRGKLFEGAFKRYKMGQIEIDQVEGLQY	720	
QY	721	LASRYFIDLDRGIGHSYGYLSLALMQRSDIFRVAIAGAPVLMIFYDTGTERYV	780	
DB	721	LASRYFIDLDRGIGHSYGYLSLALMQRSDIFRVAIAGAPVLMIFYDTGTERYV	780	
QY	781	GHPDQEGYVIGSVAMQAEKFPSEPNRLLLHGFIDENVFAHTSILISFLVRAKRPV	840	
DB	781	GHPDQEGYVIGSVAMQAEKFPSEPNRLLLHGFIDENVFAHTSILISFLVRAKRPV	840	
QY	841	LQIYPOERHSIRVESGEHYELHLHYLOENLGSRTAALKVI	882	
DB	841	LQIYPOERHSIRVESGEHYELHLHYLOENLGSRTAALKVI	882	

RESULT 3
ABG61591
ID ABG61591 standard; Protein: 882 AA.
XX
AC ABG61591;
XX
DT 12-AUG-2002 (first entry)

XX	DE	Human DPPIV related serine protease DPP-1.
XX	KW	Human; serine protease; dipeptidyl peptidase IV-related protein; DPP;
XX	KW	DPPV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
XX	KW	diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
XX	KW	heart failure; hypertension; urinary retention; osteoporosis; cancer;
XX	KW	ulcer; allergy; cancer; psychotic disorder; neurological disorder;
XX	KW	dyskinesia; reproductive disorder; inflammatory disorder;
XX	metabolic disorder.	
OS	Homo sapiens.	
XX	W0200231134-A2.	
XX	18-APR-2002.	
XX	12-OCT-2001; 2001WO-US31874.	
XX	12-OCT-2000; 2000US-240117P.	
XX	(FERR) FERRING BV.	
PI	Qi S, Akinsanya KO, Riviere PJ, Junien J;	
XX	WPI; 2002-444178/47.	
DR	N-PSDB; ABK83322.	
XX	New, dipeptidyl peptidase IV-related proteins and nucleic acids encoding	
PT	the proteins, useful for treating e.g. fungal, bacterial, protozoan and	
PT	viral infections, cancers, allergies, neurological disorders, or pain	
PT	-	
PS	Claim 17; Fig 1; 113pp; English.	
XX	The present invention relates to the isolation of novel human serine	
CC	proteases referred to as dipeptidyl peptidase IV (DPPV)-related	
CC	proteins (DPPP). The dipeptidyl peptidase IV-related proteins (DPPP)	
CC	and nucleic acids encoding them are useful for treating infections	
CC	such as fungal, bacterial, protozoan and viral infections, particularly	
CC	infections caused by human immunodeficiency virus (HIV-1 or HIV-2),	
CC	pain, diabetes, precocious puberty, infertility, obesity, anorexia,	
CC	bulimia, Parkinson's disease, acute heart failure, hypotension,	
CC	hypertension, urinary retention, osteoporosis, angina pectoris,	
CC	stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,	
CC	psychotic and neurological disorders (e.g. anxiety, dementia, or	
CC	schizophrenia), and dyskinesias. These may also be used in discovering	
CC	therapeutic agents for the treatment of reproductive, inflammatory and	
CC	metabolic disorders. ABG61591-ABG61612 represent human DPP proteins.	
XX	Sequence 882 AA;	
SO		
	Query Match	100.0%; Score 4700; DB 23; Length 882;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 882; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MAAMETBOLGVIFETADCEENIESODRPKLEPFYVERYSMSQLKLLADTRKRYGYM 60
DB	1	MAAMETBOLGVIFETADCEENIESODRPKLEPFYVERYSMSQLKLLADTRKRYGYM 60
QY	61	AKAPHDEPFVKRRNDPGPHSDRIYYLAMSGENRENTLFYSEIKPTINRAAVLMLSKPLL 120
DB	61	AKAPHDEPFVKRRNDPGPHSDRIYYLAMSGENRENTLFYSEIKPTINRAAVLMLSKPLL 120
QY	121	DLFOATLDYGMTSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180
DB	121	DLFOATLDYGMTSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180
QY	181	FTQOPLRPNLVEISCPNIRMDPKLCPADPDMIAFIHNSNDIWNISNIYTRERRLTYVHNEL 240
DB	181	FTQOPLRPNLVEISCPNIRMDPKLCPADPDMIAFIHNSNDIWNISNIYTRERRLTYVHNEL 240
QY	241	ANNEEDARSAGVATFVLOEEFDRTSGYWMCKPAAETTPSGGKILRLIYEENDESEVEIHY 300

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|||||
Db 241 ANNEEDARSAGVATFVLOEEFDRSGYWMCPKATETPSGKILRILEYENDESEVEIHHV 300
OY 301 TSPMLETRRADSFRRYPKTGANKPVTFKMSIMIDAGRIIIVDKLLOPFEILFEGVE 360
Db 301 TSPMLETRRADSFRRYPKTGANKPVTFKMSIMIDAGRIIIVDKLLOPFEILFEGVE 360
OY 361 YIARAGTPEGKYAMSIILDRSOTRLOIYLISPELFPVEDDWERORLIESVDSYTPL 420
Db 361 YIARAGTPEGKYAMSIILDRSOTRLOIYLISPELFPVEDDWERORLIESVDSYTPL 420
OY 421 IYEEETDWINIHDIHFVHPQSHHEEIEFIASECTGFRHLKYKTSILKESYKRSSG 480
Db 421 IYEEETDWINIHDIHFVHPQSHHEEIEFIASECTGFRHLKYKTSILKESYKRSSG 480
OY 481 GLPAPSDFKCPIKEELAITSGEWEVLGRHGSNTIOVDEVRLVYFEGTKDSPLEHHLVVS 540
Db 481 GLPAPSDFKCPIKEELAITSGEWEVLGRHGSNTIOVDEVRLVYFEGTKDSPLEHHLVVS 540
OY 541 YVNPGEVTRLMDRGYSHSCCISOHCDFISKYSNKNPHCVSLKLSPEDDPTCKTEF 600
Db 541 YVNPGEVTRLMDRGYSHSCCISOHCDFISKYSNKNPHCVSLKLSPEDDPTCKTEF 600
OY 601 WATILDSAGLPDYTPPEITFSFESTGTLYKMLYKPHDLOPKKYPVLFYIGPOVOL 660
Db 601 WATILDSAGLPDYTPPEITFSFESTGTLYKMLYKPHDLOPKKYPVLFYIGPOVOL 660
OY 661 VNNRFEKVKFRLNTLASLGVVVVINDRSGCHRGKFECAFYKFKMOIIEIDDOVEGLQY 720
Db 661 VNNRFEKVKFRLNTLASLGVVVVINDRSGCHRGKFECAFYKFKMOIIEIDDOVEGLQY 720
OY 721 LASRYDEIDLDVRIHGMSTGYGLSLMALMQRSDIFRVAIAGAPVTLMIFYDGYTERYM 780
Db 721 LASRYDEIDLDVRIHGMSTGYGLSLMALMQRSDIFRVAIAGAPVTLMIFYDGYTERYM 780
OY 781 GHPPONOGYVLGSAVQAQKFPSEPRNLLHGFLENNHFAITSLISTVLAAGRPYD 840
Db 781 GHPPONOGYVLGSAVQAQKFPSEPRNLLHGFLENNHFAITSLISTVLAAGRPYD 840
OY 841 LQIYPERHSIRVPESEGEHELHLHYLOENLGSRIALKVI 882
Db 841 LQIYPERHSIRVPESEGEHELHLHYLOENLGSRIALKVI 882

RESULT 4
AAU74749
ID AAU74749 standard; Protein: 882 AA.
XX
AC AAU74749;
XX
DT 09-APR-2002 (first entry)
XX
DE Human protease PR7S-9 protein sequence.
XX
KW Human; protease; PR7S; gastrointestinal; Crohn's disease; cancer;
KW cardiovascular; atherosclerosis; autoimmune disorder; dermatitis;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW cell proliferative disorder; developmental disorder; epilepsy;
KW Duchenne muscular dystrophy; epithelial disorder; neurological disorder;
KW reproductive disorder; endometriosis.
XX
OS Homo sapiens.
XX
PN MO200198468-A2.
XX
PD 27-DEC-2001.
XX
PF 13-JUN-2001; 2001MO-US19178.
XX
PR 16-JUN-2000; 2000US-212336P.
PR 22-JUN-2000; 2000US-213955P.
PR 29-JUN-2000; 2000US-215336P.
PR 07-JUL-2000; 2000US-216821P.
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PR 14-JUL-2000; 2000US-218946P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM;
PI Deleage AM, Baughn MR, Nguyen DB, Lee EA, Hatalla A, Khan FA;
PI Walla NK, Yao MG, Lu DM, Patterson C, Tang YT, Walsh RT;
PI Azimzai Y, Lu Y, Rankumar J, Xu Y, Reddy R, Das D, Kearney L;
PI Kallick DA;
XX
DR WPI: 2002:090437/12.
DR N-PSDB; ABK12892.
XX
PT Twenty one human proteases (referred to as PR7S-1 to PR7S-21), useful
PT in the diagnosis, treatment and prevention of gastrointestinal (e.g.
PT gastritis), cardiovascular (e.g. atherosclerosis) and cell
PT proliferative (e.g. cancer) disorders.
XX
PS Claim 1; Page 140-142; 177pp; English.
XX
CC The present invention relates to twenty one new human proteases,
CC referred to as PR7S-1 to PR7S-21. The PR7S polynucleotides and
CC polypeptides of the invention are useful in the diagnosis, treatment and
CC prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and
CC Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and
CC myocardial infarction, autoimmune/inflammatory e.g. acquired
CC immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell
CC proliferative e.g. cancer, developmental e.g. Duchenne and Becker
CC muscular dystrophy, epithelial e.g. dermatitis, neurological e.g.
CC epilepsy and Alzheimer's disease and reproductive e.g. infertility and
CC endometriosis disorders. Numerous other examples of each disorder are
CC given in the specification. The present protein sequence represents
CC the human protease PR7S-9 protein of the invention.
XX
SQ Sequence 882 AA;
Query Match 100.0%; Score 4700; DB 23; Length 882;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAAMETEOIGVEFFFADEENIESODRKLPEFYERYSMWOLKLLADTRKYHYGM 60
Db 1 MAAMETEOIGVEFFFADEENIESODRKLPEFYERYSMWOLKLLADTRKYHYGM 60
OY 61 AKAPHDFMFKRNDPDSGPHSDRIYLLAMSGENRENTLFYEIPIKTINRAAVLMSKPL 120
Db 61 AKAPHDFMFKRNDPDSGPHSDRIYLLAMSGENRENTLFYEIPIKTINRAAVLMSKPL 120
OY 121 DLFOATLDYGMYSREBELREKRKIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180
Db 121 DLFOATLDYGMYSREBELREKRKIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180
OY 181 FTQOPLRPNIIVERTSCPINRMDPKICPADPDWIAFIHSDNDIWSINIVREERRLLTYVNEL 240
Db 181 FTQOPLRPNIIVERTSCPINRMDPKICPADPDWIAFIHSDNDIWSINIVREERRLLTYVNEL 240
OY 241 ANNEEDARSAGVATFVLOEEFDRSGYWMCPKATETPSGKILRILEYENDESEVEIHHV 300
Db 241 ANNEEDARSAGVATFVLOEEFDRSGYWMCPKATETPSGKILRILEYENDESEVEIHHV 300
OY 301 TSPMLETRRADSFRRYPKTGANKPVTFKMSIMIDAGRIIIVDKLLOPFEILFEGVE 360
Db 301 TSPMLETRRADSFRRYPKTGANKPVTFKMSIMIDAGRIIIVDKLLOPFEILFEGVE 360
OY 361 YIARAGTPEGKYAMSIILDRSOTRLOIYLISPELFPVEDDWERORLIESVDSYTPL 420
Db 361 YIARAGTPEGKYAMSIILDRSOTRLOIYLISPELFPVEDDWERORLIESVDSYTPL 420
OY 421 IYEEETDWINIHDIHFVHPQSHHEEIEFIASECTGFRHLKYKTSILKESYKRSSG 480
Db 421 IYEEETDWINIHDIHFVHPQSHHEEIEFIASECTGFRHLKYKTSILKESYKRSSG 480
OY 481 GLPAPSDFKCPIKEELAITSGEWEVLGRHGSNTIOVDEVRLVYFEGTKDSPLEHHLVVS 540
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Db	721	LASRFDFIDLRVGHGHSYGGYISTLWALMQRSDIFFEVALAGAPVTLMIRYDGYERFM	780
Oy	761	GHPDNEGGYILGSVAMQAEKFPSEPNRLLLHGFEDENVAFTSILLSPFLVRACKPYD	840
Db	781	GHPDNEGGYILGSVAMQAEKFPSEPNRLLLHGFEDENVAFTSILLSPFLVRACKPYD	840
Oy	841	LQIYPQERHSIRVPESGEHYELHLHYLOENVLGSRIAAIKVI	882
Db	841	LQIYPQERHSIRVPESGEHYELHLHYLOENVLGSRIAAIKVI	882
<hr/>			
RESULT 6			
ABR97361			
Xx	ID	ABR97361 standard; Protein: 782 AA.	
Xx	AC		
Xx	ABR97361;		
Xx	DT		
Xx	27-JUN-2002 (first entry)		
Xx			
Xx	Novel human protein SEQ ID NO: 629.		
Xx			
Kw	Human; anti-naeemic; vulnerary; anti-inflammatory; immunomodulator;		
Kw	antifertility; cerebroprotective; cytosolic; rheumatic; gene therapy;		
Kw	neuroprotective; antiparkinsonian; protein therapy; Estf;		
Kw	expressed sequence tag.		
Xx			
Os	Homo sapiens.		
Pn	MO200222660-A2.		
Xx			
Pd	21-MAR-2002.		
Pf	10-SEP-2001; 2001WO-US26015.		
Pr	11-SEP-2000; 2000US-0659671.		
Xx			
Pa	(HYSE-) HYSEQ INC.		
Xx			
Pi	Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;		
Pi	Xue AJ, Yang Y, Wehrman T, Dimaac RT;		
Xx			
Dk	WPI: 2002-292408/73.		
Dk	N-PsDB: ABR32547.		
Xx			
Pt	An isolated polynucleotide for treating diseases associated with its		
Pt	encoded polypeptide such as cancer and multiple sclerosis -		
Xx			
Pt	Example 2: SEQ ID NO 629; 509pp; English.		
Xx			
Cc	The present invention provides the protein and coding sequences of 444		
Cc	novel human proteins. These were isolated from expressed sequences tags		
Cc	(ESTs). They can be used to stimulate cell growth, to regulate		
Cc	haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth		
Cc	e.g. in burn treatment, to regulate the immune system e.g. to treat		
Cc	multiple sclerosis, to regulate activin or inhibin e.g. to treat		
Cc	fertility, to regulate haemostasis or thrombolysis e.g. to treat		
Cc	stroke and cancer, to screen for drugs, to treat inflammatory conditions		
Cc	e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.		
Cc	Parkinson's disease. The present sequence is a protein of the invention.		
Xx			
Xx	Sequence 782 AA:		
<hr/>			
Query Match	87.6%; Score 4118; DB 23; Length 782;		
Best Local Similarity	88.7%; Pred. No. 0;		
Matches 782; Conservative	0; Mismatches 0; Indels 100; Gaps		
Oy	1 MAAMETQLGVLEIFETADCEENIESODRPKLPEFFYERYSWSOLKKLADTRKRYHGVM	60	
Db	1 MAAMETQLGVLEIFETADCEENIESODRPKLPEFFYERYSWSOLKKLADTRKRYHGVM	60	
Oy	AKAPHEDEFVRRNDPDGSHSRIRYYLAANGRENTLFYSIRPTINRAAVMLSKPPL	120	
Db	AKAPHEDEFVRRNDPDGSHSRIRYYLAANGRENTLFYSIRPTINRAAVMLSKPPL	120	

Db	61	AKAPHDPEFVKRNDPDGPHSDRIYYLLAMSGENRENTLFYEISPKTINRAAVLMLSNKPLL	120
QY	121	DLFOATLDYGMYSREBELLRERKRTIGYTAISYVHOGSGTFPLFQAGSGIYHNKDGPGQ	180
Db	121	DLFOATLDYGMYSREBELLRERKRTIGYTAISYVHOGSGTFPLFQAGSGIYHNKDGPGQ	180
QY	181	FTQOGLRNLVETSCPNIRMDPKLCPADPDWIAFTHSNDIMISNIVYREERRLTYVHNEL	240
Db	181	FTQOGLRNLVETSCPNIRMDPKLCPADPDWIAFTHSNDIMISNIVYREERRLTYVHNEL	240
QY	241	ANMEDASAGVAFFVLOEEFDYSGYWCPCKAETPTPSGGKILRLIYEENDESEVEITIHV	300
Db	241	ANMEDASAGVAFFVLOEEFDYSGYWCPCKAETPTPSGGKILRLIYEENDESEVEITIHV	300
QY	301	TSPMLFTRRADSFRRPKTGTAANPKVTFRMSIMIMDAGRIIIVDIDKLLDPFELPFGVE	360
Db	301	TSPMLFTRRADSFRRPKTGTAANPKVTFRMSIMIMDAGRIIIVDIDKLLDPFELPFGVE	360
QY	361	YIARAGWTPPEGVYANSILDRSOTRLQVLISPELFTIPVEDDWERQLIESVDSVTP	420
Db	361	YIARAGWTPPEGVYANSILDRSOTRLQVLISPELFTIPVEDDWERQLIESVDSVTP	420
QY	421	IYYEETDIWINIHDFHVPQSHSEELIEFTFASECKTGFRHLKYITNLSKESYKRSSG	480
Db	421	IYYEETDIWINIHDFHVPQSHSEELIEFTFASECKTGFRHLKYITNLSKESYKRSSG	480
QY	481	GLPADSDKCPCKEELIATTSGEWEYLGRHSGNIQVDEYRRLVTFEGTKDSPLEHHLVYS	540
Db	481	GLPADSDKCPCKEELIATTSGEWEYLGRHSGNIQVDEYRRLVTFEGTKDSPLEHHLVYS	540
QY	541	YVNPEEVRRLDRGYSHSCCISQHCDFITISYSNQKNPHCVSLYKLISSPEDDPCKTKEF	600
Db	541	YVNPEEVRRLDRGYSHSCCISQHCDFITISYSNQKNPHCVSLYKLISSPEDDPCKTKEF	600
QY	601	WATILDSAGPLPDYVPELTFSESTTGTGLGMLYKPHDLQPCKKPTVLFYIGGPVOL	660
Db	601	WATILDSAGPLPDYVPELTFSESTTGTGLGMLYKPHDLQPCKKPTVLFYIGGPQ---	657
QY	661	VNNREKGVKFRRLNTLASLGIYVVVYIDNRSGSHRGLKFECAFYKIMQOIEIDDOVEGLQY	720
Db	658	-----	657
QY	721	LASRDFLIDLRVGIHGSYGGYLSIALMLQMSDIPFVATAGAPVTLMIFYDTGYTERYM	780
Db	658	-----VALTAGAVTLMIFYDTGYTERYM	860
QY	781	GHPDNEGGYLGSAVMAOEKFPSEPNRLLLHGFIDENVHFAHTSILLSFLVRAGKPYD	840
Db	681	GHPDNEGGYLGSAVMAOEKFPSEPNRLLLHGFIDENVHFAHTSILLSFLVRAGKPYD	740
QY	841	LQIYPERHSIRVPESGEHYELHLHLHYQENLGSRIALAKVI	882
Db	741	LQIYPERHSIRVPESGEHYELHLHLHYQENLGSRIALAKVI	782
RESULT 7			
ABB97362			
ID	ABB97362	standard; Protein: 724 AA.	
XX	AC	ABB97362;	
XX	DT	27-JUN-2002 (first entry)	
XX	DE	Novel human protein SEQ ID NO: 630.	
KM	XX	Human: anti-nausea; vulnerary; anti-inflammatory; immunomodulator;	
KM	XX	anti-infectivity; cerebroprotective; cytoskeletal; rheumatic; gene therapy;	
KM	XX	neuroprotective; antiparkinsonian; protein therapy; EST.	
KM	XX	expressed sequence tag.	
OS	XX	Homo sapiens.	
PN	WO200222660-A2.		


```

XX 21-MAR-2002.
PD 10-SEP-2001; 2001WO-US26015.
XX 11-SEP-2000; 2000US-0659671.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX MPI: 2002-292408/33.
XX N-PSDB; ABR32548.
XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX Example 2; SEQ ID NO 630; 509pp; English.
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention.
XX
XX Sequence 724 AA:
SQ
Query Match 80.2%; Score 3771; DB 23; Length 724;
Best Local Similarity 82.1%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 158; Gaps 2;
QY 1 MAAMETQLGVEIFETADCEENIESODRKLPEFYERYSWSQLKLLADTRKYHYGM 60
DB 1 MAAMETQLGVEIFETADCEENIESODRKLPEFYERYSWSQLKLLADTRKYHYGM 60
QY 61 AKAPHEMFYKRNDDPGPHSDRIYLLAMSGENRENTLFYSEIKTIRAVLMSKPL 120
DB 61 AKAPHEMFYKRNDDPGPHSDRIYLLAMSGENRENTLFYSEIKTIRAVLMSKPL 120
QY 121 DLFQATLDYGMYSREBELLEKRRIGTGVGIASYDHQSGTFLQAGSGYHWKDGPG 180
DB 121 DLFQATLDYGMYSREBELLEKRRIGTGVGIASYDHQSGTFLQAGSGYHWKDGPG 180
QY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWMISNIVTREERRLLTYVHNL 240
DB 125 --QQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWMISNIVTREERRLLTYVHNL 182
QY 241 ANNEEDARSAGVATFVLQEEFDYSGYWCMPKATTPSGKILRLYLENDESEVELIHY 300
DB 183 ANNEEDARSAGVATFVLQEEFDYSGYWCMPKATTPSGKILRLYLENDESEVELIHY 242
QY 301 TSPMLETRADSRFRYKTKGTANKYTFKMSIIMADAGRIIDVYDKLIOPFELFGVGE 360
DB 243 TSPMLETRADSRFRYKTKGTANKYTFKMSIIMADAGRIIDVYDKLIOPFELFGVGE 302
QY 361 YIIRAGTPEGKAWMSILLDRSOTRLQIYLISELFIPEVDVWERQRLIESVDSVTP 420
DB 303 YIIRAGTPEGKAWMSILLDRSOTRLQIYLISELFIPEVDVWERQRLIESVDSVTP 362
QY 421 IITEETDIIINHDIFHVHPQSHHEEIEFIASECTGGRHLKITSILKESKYKSSG 480
DB 363 IITEETDIIINHDIFHVHPQSHHEEIEFIASECTGGRHLKITSILKESKYKSSG 422
QY 481 GLPAPDFKCPKEELATITSGEWEVLGRHGSNIQVDEVRRLVFEFGKDSPLEHLLTVS 540
DB 423 GLPAPDFKCPKEELATITSGEWEVLGRHGSNIQVDEVRRLVFEFGKDSPLEHLLTVS 482

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QY 541 YVNPGEVTRLDRGYSHSCISQHCDFISKYSNOKNPHCVSLYKLSPEDDPTCKTEF 600
DB 483 YVNPGEVTRLDRGYSHSCISQHCDFISKYSNOKNPHCVSLYKLSPEDDPTCKTEF 542
QY 601 WATILDSAGPLPDYTPPEIFESFESTGTFTLYGMLYKPHDLOPGKKYPTVLFTYGGPOVOL 660
DB 543 WATILDSAGPLPDYTPPEIFESFESTGTFTLYGMLYKPHDLOPGKKYPTVLFTYGGPOVOL 599
QY 661 VNNRKCVMYFRLMTLASLQYVVVVIDNRGSCRHGLKFEQAFYKMKQIEIDQVDELQY 720
DB 600 ----- 599
QY 721 LASHYDFIDLRVINGMSYGYLSLMAQLMSQDIFRVAIAGAPVTLMFYDTGYTERYM 780
DB 600 -----VALIAGAPVTLMFYDTGYTERYM 622
QY 781 GHPDNEGGYLLGSVAMQAEKFPSEPRKLLHGFLENVHFATSTILSLFLVRAGKPYD 840
DB 623 GHPDNEGGYLLGSVAMQAEKFPSEPRKLLHGFLENVHFATSTILSLFLVRAGKPYD 682
QY 841 LQIYPOERHSIRVSEGEHELHLHYLOENLGRIALKVI 882
DB 683 LQIYPOERHSIRVSEGEHELHLHYLOENLGRIALKVI 724
RESULT 8
ABG61600
ID ABG61600 standard; Protein: 658 AA.
AC ABG61600;
XX
XX 12-AUG-2002 (first entry)
XX
XX Human DPPP-1 splice variant #7.
XX
XX Human: serine protease: dipeptidyl peptidase IV-related protein; DPPP;
XX DPPIV; infection: human immunodeficiency virus; HIV-1; HIV-2; pain;
XX diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
XX heart failure; hypertension; urinary retention; osteoporosis; cancer;
XX ulcer; allergy; cancer; psychotic disorder; neurological disorder;
XX dyskinesia; reproductive disorder; inflammatory disorder;
XX metabolic disorder.
XX
XX Homo sapiens.
XX
XX WO200231134-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US31874.
XX
XX 12-OCT-2000; 2000US-240117P.
XX
XX (FERR) FERRING BV.
XX
XX Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX MPI: 2002-444178/47.
XX N-PSDB; ABR3331.
XX
XX New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
XX the proteins, useful for treating e.g. fungal, bacterial, protozoan and
XX viral infections, cancers, allergies, neurological disorders, or pain
XX
XX Disclosure: Page 70-72; 113pp; English.
XX
XX The present invention relates to the isolation of novel human serine
XX proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
XX proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
XX and nucleic acids encoding them are useful for treating infections
XX such as fungal, bacterial, protozoan and viral infections, particularly
XX infections caused by human immunodeficiency virus (HIV-1 or HIV-2),

```

CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.

XX Sequence 658 AA:

Query Match 74.6%; Score 3504; DB 23; Length 658;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAMETEOGLVEFEETADCEENIESODRKLPEFYERYSMSOLKLLADTRKYHYGM 60
 DB 1 MAAMETEOGLVEFEETADCEENIESODRKLPEFYERYSMSOLKLLADTRKYHYGM 60
 OY 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBRENTLFYSEIKPTIRAAVLMLSKPL 120
 DB 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBRENTLFYSEIKPTIRAAVLMLSKPL 120
 OY 121 DLFOATLDYGMYSREBELLEBRKRIGVGLASYDYHOGSGTFLFOAGSGIYHVKGDPQG 180
 DB 121 DLFOATLDYGMYSREBELLEBRKRIGVGLASYDYHOGSGTFLFOAGSGIYHVKGDPQG 180
 OY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPMIAFIHSDNIMISNIVREERRLLTYVNNEL 240
 DB 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPMIAFIHSDNIMISNIVREERRLLTYVNNEL 240
 OY 241 ANMEDARSAGVATFVLOEEDRYSYGMWCPKAEPTPSGKILRIILENDESEVEIITHV 300
 DB 241 ANMEDARSAGVATFVLOEEDRYSYGMWCPKAEPTPSGKILRIILENDESEVEIITHV 300
 OY 301 TSPLELERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIQFELLFEGVE 360
 DB 301 TSPLELERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIQFELLFEGVE 360
 OY 361 YIARAGTPEKGYAMSLILDBSOTRLQIVLISPELFIPEVDVNERORLISVDSVTPL 420
 DB 361 YIARAGTPEKGYAMSLILDBSOTRLQIVLISPELFIPEVDVNERORLISVDSVTPL 420
 OY 421 IYETTDIWINIHIDIFHVEPQSHHEEIEFLFASCECTGFRHLKITSILKESKYKSSG 480
 DB 421 IYETTDIWINIHIDIFHVEPQSHHEEIEFLFASCECTGFRHLKITSILKESKYKSSG 480
 OY 481 GLPAPSDFOKCIKEIATITSGEWEVLGRHGSNIQVDEVRRLLVYEGTQSDPLEHLLYVVS 540
 DB 481 GLPAPSDFOKCIKEIATITSGEWEVLGRHGSNIQVDEVRRLLVYEGTQSDPLEHLLYVVS 540
 OY 541 YVNGEYTRLDRGYSHSCCISQHCDEFISKYSNOKNPHCSLYKLSPEDDPCKTKEF 600
 DB 541 YVNGEYTRLDRGYSHSCCISQHCDEFISKYSNOKNPHCSLYKLSPEDDPCKTKEF 600
 OY 601 WATILDSAGLPDYTPPELIFSESTGTGLYGLMKLPHDLOPKKYPVLTFIYGG 655
 DB 601 WATILDSAGLPDYTPPELIFSESTGTGLYGLMKLPHDLOPKKYPVLTFIYGG 655

RESULT 9

ABG61596 ID ABG61596 standard; Protein; 661 AA.

XX AC ABG61596;

XX 12-AUG-2002 (first entry)

XX Human DPRP-1 splice variant #3.

KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPY; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;

KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.

XX Homo sapiens.

PN WO200231134-A2.

PD 18-APR-2002.

PE 12-OCT-2001; 2001WO-US31874.

PR 12-OCT-2000; 2000US-240117P.

XX (FERR) FERRING BV.

PI Q1 S, Atkinsanya KO, Riviere PJ, Junten J;

DR WPI; 2002-444178/47.

DR N-PSDB; ABK83327.

PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 XX

XX Disclosure; Page 63-65; 113pp; English.

XX The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPY)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
 CC

XX Sequence 661 AA:

Query Match 74.6%; Score 3504; DB 23; Length 661;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAMETEOGLVEFEETADCEENIESODRKLPEFYERYSMSOLKLLADTRKYHYGM 60
 DB 1 MAAMETEOGLVEFEETADCEENIESODRKLPEFYERYSMSOLKLLADTRKYHYGM 60
 OY 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBRENTLFYSEIKPTIRAAVLMLSKPL 120
 DB 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBRENTLFYSEIKPTIRAAVLMLSKPL 120
 OY 121 DLFOATLDYGMYSREBELLEBRKRIGVGLASYDYHOGSGTFLFOAGSGIYHVKGDPQG 180
 DB 121 DLFOATLDYGMYSREBELLEBRKRIGVGLASYDYHOGSGTFLFOAGSGIYHVKGDPQG 180
 OY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPMIAFIHSDNIMISNIVREERRLLTYVNNEL 240
 DB 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPMIAFIHSDNIMISNIVREERRLLTYVNNEL 240
 OY 241 ANMEDARSAGVATFVLOEEDRYSYGMWCPKAEPTPSGKILRIILENDESEVEIITHV 300
 DB 241 ANMEDARSAGVATFVLOEEDRYSYGMWCPKAEPTPSGKILRIILENDESEVEIITHV 300
 OY 301 TSPLELERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIQFELLFEGVE 360
 DB 301 TSPLELERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIQFELLFEGVE 360

OY 361 YIARAGWTPGKGYAMSLILDRSQRLOIVLISPELFIPEDDVNERORLIESVPSVPL 420
 DB 361 YIARAGWTPGKGYAMSLILDRSQRLOIVLISPELFIPEDDVNERORLIESVPSVPL 420
 OY 421 IYEEETDWINHIDHIFVPOSHHEEIEFIASECKTGRHLKITSILKESYKRSSG 480
 DB 421 IYEEETDWINHIDHIFVPOSHHEEIEFIASECKTGRHLKITSILKESYKRSSG 480
 OY 481 GLPAPSPDKCPKEIEIATITSGEMEVLRHGSNIQVDEVRRLVFEGRKDSPLEHHLVVS 540
 DB 481 GLPAPSPDKCPKEIEIATITSGEMEVLRHGSNIQVDEVRRLVFEGRKDSPLEHHLVVS 540
 OY 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQNPHCVSLYKLSPEDDPTCKTKEF 600
 DB 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQNPHCVSLYKLSPEDDPTCKTKEF 600
 OY 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLOPKKYPVLFYIGG 655
 DB 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLOPKKYPVLFYIGG 655

RESULT 10

ABG61594
 ID ABG61594 standard; Protein: 690 AA.

AC ABG61594:

DT 12-AUG-2002 (first entry)

DE Human DPP-1 splice variant #1.

XX Human DPP-1 splice variant #1.
 XX DPP-1, infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 XX diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 XX heart failure; hypertension; urinary retention; osteoporosis; cancer;
 XX ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 XX dyslexia; reproductive disorder; inflammatory disorder;
 XX metabolic disorder.

OS Homo sapiens.

PN WO200231134-A2.

PD 18-APR-2002.

PF 12-OCT-2001: 2001MO-US31874.

PR 12-OCT-2000: 2000US-240117P.

PA (FERR) FERRING BV.

PI Q1 S, Akimsanya KO, Riviere PJ, Junten J;

DR WPI: 2002-444178/47.

DR N-PSDB; ABR83325.

XX New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain

PS Disclosure: Page 59-61; 113pp; English.

XX The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related
 CC proteins (DPP-IV). The dipeptidyl peptidase IV-related proteins (DPP-IV)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bullma, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris.

CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyslexias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPP proteins.

XX Sequence 690 AA;

Query Match 74.6%; Score 3504; DB 23; Length 690;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAMETEOGLVEIETADCEENIESQDRPKLEPFYERYYSWSOLKLLADTRKHGM 60
 DB 1 MAAMETEOGLVEIETADCEENIESQDRPKLEPFYERYYSWSOLKLLADTRKHGM 60.

OY 61 AKAPHDMEFVKRNDPDGPHSDRIYLLAMSGENRENTLFSEIPTINRAAVLMSKPL 120
 DB 61 AKAPHDMEFVKRNDPDGPHSDRIYLLAMSGENRENTLFSEIPTINRAAVLMSKPL 120

OY 121 DLFOATLDYGYMREELREKRIGTVGIASVDYHOGSGTFLQAGSGIYHVKDGPG 180
 DB 121 DLFOATLDYGYMREELREKRIGTVGIASVDYHOGSGTFLQAGSGIYHVKDGPG 180

OY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIMISNIVREERLLYVHNL 240
 DB 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIMISNIVREERLLYVHNL 240

OY 241 ANMEDARSAGVATFVLOEEDRISGYWMCRAETTPSGGKILKILVENESEVEIIV 300
 DB 241 ANMEDARSAGVATFVLOEEDRISGYWMCRAETTPSGGKILKILVENESEVEIIV 300

OY 301 TSPULETRRADSFYPTGTANPKVTFKMSIMIDAEGRIIDVIDKELIOFELLFEGVE 360
 DB 301 TSPULETRRADSFYPTGTANPKVTFKMSIMIDAEGRIIDVIDKELIOFELLFEGVE 360

OY 361 YIARAGWTPGKGYAMSLILDRSQRLOIVLISPELFIPEDDVNERORLIESVPSVPL 420
 DB 361 YIARAGWTPGKGYAMSLILDRSQRLOIVLISPELFIPEDDVNERORLIESVPSVPL 420

OY 421 IYEEETDWINHIDHIFVPOSHHEEIEFIASECKTGRHLKITSILKESYKRSSG 480
 DB 421 IYEEETDWINHIDHIFVPOSHHEEIEFIASECKTGRHLKITSILKESYKRSSG 480

OY 481 GLPAPSPDKCPKEIEIATITSGEMEVLRHGSNIQVDEVRRLVFEGRKDSPLEHHLVVS 540
 DB 481 GLPAPSPDKCPKEIEIATITSGEMEVLRHGSNIQVDEVRRLVFEGRKDSPLEHHLVVS 540

OY 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQNPHCVSLYKLSPEDDPTCKTKEF 600
 DB 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQNPHCVSLYKLSPEDDPTCKTKEF 600

OY 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLOPKKYPVLFYIGG 655
 DB 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLOPKKYPVLFYIGG 655

RESULT 11

AAB93565
 ID AAB93565 standard; Protein: 632 AA.

AC AAB93565:

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:12964.

XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

XX EPI074617-A2.

PD 07-FEB-2001.
 XX
 PE 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 12964; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 XX
 SQ Sequence 632 AA:
 Query Match 70.9%; Score 3333.5; DB 22; Length 632;
 Best Local Similarity 92.4%; Pred. No. 2.3e-312;
 Matches 631; Conservative 0; Mismatches 1; Indels 51; Gaps 1;
 1;
 QY 200 MDPKLCPADPDMWIAFIHNDIWNISVITREERLTYVNELANMEDARSGAVTFVLOE 259
 DB 1 MDPKLCPADPDMWIAFIHNDIWNISVITREERLTYVNELANMEDARSGAVTFVLOE 60
 QY 260 EFDRTSGYMWCPKATETPSSGKILRLIYEENDESEVELIHTSPMLERRADSEFYPTG 319
 DB 61 EFDRTSGYMWCPKATETPSSGKILRLIYEENDESEVELIHTSPMLERRADSEFYPTG 120
 QY 320 TANPKVTFKMEIMIDAGRIIDVADKELIOPFELIFGVEYIARAGTPEGKYAMSTLL 379
 DB 121 TANPKVTFKMEIMIDAGRIIDVADKELIOPFELIFGVEYIARAGTPEGKYAMSTLL 180
 QY 380 DRSGTRLOIVILSPPLFVDEDDVMERQRLIESVPDVSPTPLIYEETDININHIDFHV 439
 DB 181 DRSGTRLOIVILSPPLFVDEDDVMERQRLIESVPDVSPTPLIYEETDININHIDFHV 240
 QY 440 FPOSHHEIEIFPASECTGFRHLKYITSLIKESKYRSSGGLPAPSPFKPIKEEIT 499
 DB 241 FPOSHHEIEIFPASECTGFRHLKYITSLIKESKYRSSGGLPAPSPFKPIKEEIT 300

QY 500 SGMEVVLGRHSGNIQVDEVRLVYEEGTQDSPLEHHLVVSYNVGEVTRLTDRGYSHSC 559
 DB 301 SGMEVVLGRHSGNIQVDEVRLVYEEGTQDSPLEHHLVVSYNVGEVTRLTDRGYSHSC 360
 QY 560 CISOHCDEFISKYSNOKNPHCVSLKLSPPDDPCKTKEWATITLSAGLPDYTPPEI 619
 DB 361 CISOHCDEFISKYSNOKNPHCVSLKLSPPDDPCKTKEWATITLSAGLPDYTPPEI 420
 QY 620 FSPSTGTFTLYGMLYKPHDLOPGKKYPTVLFYGGPOVOLVNNRFKVKERLNTLASL 679
 DB 421 FSPSTGTFTLYGMLYKPHDLOPGKKYPTVLFYGGPOVOLVNNRFKVKERLNTLASL 480
 QY 680 GYVVVVVDNRGSCRHGLTFEGAFYKKMGQLEIDDQEGLOYLASRYDFIDLRVGHWS 739
 DB 481 GYVVVVVDNRGSCRHGLTFEGAFYKKMGQLEIDDQEGLOYLASRYDFIDLRVGHWS 507
 QY 740 YGCVTLSTALMQRSDIFPVATAGAPVTLWITYDYTERVYNGHPDONOGYLLCSVMOA 799
 DB 508 -----VAIAGAPVTLWITYDYTERVYNGHPDONOGYLLCSVMOA 549
 QY 800 EKFPSEPNRLLLHGFIDENVHFAHTSTLSGLVRAGKPYDLOIYPOERHSIRVPESGEH 859
 DB 550 EKFPSEPNRLLLHGFIDENVHFAHTSTLSGLVRAGKPYDLOIYPOERHSIRVPESGEH 609
 QY 860 YELHLHLYQENLGSRIAALKVI 882
 DB 610 YELHLHLYQENLGSRIAALKVI 632
 RESULT 12
 ABG61601
 ID ABG61601 standard; Protein; 613 AA.
 XX
 AC ABG61601;
 XX
 DT 12-AUG-2002 (first entry)
 XX
 DE Human DPRP-1 splice variant #8.
 XX
 KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyslexia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200231134-A2.
 PN
 PD 18-APR-2002.
 XX
 XX 12-OCT-2001; 2001WO-US31874.
 PF
 PR 12-OCT-2000; 2000US-240117P.
 PR
 PA (FERR) FERRING BV.
 PA
 PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
 PI
 XX
 DR WPI; 2002-444178/47.
 DR
 DR N-PSDB; ABK83332.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT
 PS Disclosure; Page 73-75; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related

Db 713 ORGLRFEGLAKNMGVEIEDQVEGLQFAEKYGFIDLSRVAIHGWSYGGFLSLMGLINK 772
 QY 753 SDIFRAVAGAPVTLWIFDGTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 812
 Db 773 POVFVAIAGAPVTVMAVDGTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 832
 QY 813 HGFLEDNVHFAHTSILSLFLVAGKPYDLOIYPOERHSIRVSGEYELHLHYLOENL 872
 Db 833 HGFLEDNVHFAHTSILSLFLVAGKPYDLOIYPOERHSIRVSGEYELHLHYLOENL 892

RESULT 15
 ABG61604
 ID ABG61604 standard; Protein: 892 AA.
 AC ABG61604;
 DT 12-AUG-2002 (first entry)
 DE Human DPRP-2 splice variant #3.

Human: serine protease; dipeptidyl peptidase IV-related protein; DPP; DPP1V; Infection; human immunodeficiency virus; HIV-1; HIV-2; pain; diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke; heart failure; hypertension; urinary retention; osteoporosis; cancer; ulcer; allergy; cancer; psychotic disorder; neurological disorder; dyskinetic; reproductive disorder; inflammatory disorder; metabolic disorder.

OS Homo sapiens.
 PN MO200231134-A2.
 PD 18-APR-2002.
 PF 12-OCT-2001; 2001WO-US31874.
 PR 12-OCT-2000; 2000US-240117P.
 PA (FERR) FERRING BV.
 PI Q1 S, Akinsanya KO, Riviere PJ, Junten J;
 DR WPI: 2002-444178/47.
 DR N-PSDB; ABK83335.

New dipeptidyl peptidase IV-related proteins and nucleic acids encoding the proteins, useful for treating e.g. fungal, bacterial, protozoan and viral infections, cancers, allergies, neurological disorders, or pain

Disclosure: Page 81-84; 113pp; English.

The present invention relates to the isolation of novel human serine proteases referred to as dipeptidyl peptidase IV (DPP1V)-related proteins (DPP1V). The dipeptidyl peptidase IV-related proteins (DPP1V) and nucleic acids encoding them are useful for treating infections such as fungal, bacterial, protozoan and viral infections, particularly infections caused by human immunodeficiency virus (HIV-1 or HIV-2), pain, diabetes, precocious puberty, infertility, obesity, anorexia, bulimia, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, stroke, ulcers, asthma, allergies, cancers, migraine, vomiting, psychotic and neurological disorders (e.g. anxiety, dementia, or schizophrenia), and dyskinetic. These may also be used in discovering therapeutic agents for the treatment of reproductive, inflammatory and metabolic disorders. ABG61591-ABG61612 represent human DPP1V proteins.

Sequence 892 AA:

Query Match 61.1%; Score 2870; DB 23; Length 892;
 Best Local Similarity 61.5%; Pred. NO. 2.4e-267;

Matches 517; Conservative 134; Mismatches 187; Indels 2; Gaps 2;

QY 35 FYVERYSMSQLKLLADTETKYGYMAKAPHDMPFKRNDPGRPSDRITYLALMSENRE 94
 Db 53 FOYQKSHWDGLKSLIHGSKYSGLLVNAKAPHDFOEQKTDSEGPSHRLYLYGMPYGSRE 112
 QY 95 NTLFVSEIPKTTINRAVLAWSKPLDLFOATLDGMYGREBELLEERRIGTVGIASVD 154
 Db 113 NSLKYSEIKKVKRKEALLLSKQMDHFOATPHNHGVYREBELLEERRIGTVGIASVD 172
 QY 155 YHOGSTFLFOAGSGTYHYKDGPGFTQOPLRPNLVETSCPNIMDKPLADPDMIAF 214
 Db 173 FHSEGLFLFOASNSLFCRDCGKNGFNWSPKPLEIKTQCGPRDPKICADPAFFSF 232
 QY 215 IHSNDIWINIYTRERRLTYVHNELANNEPBARSGVATPVLOEEDFSGVWMPKAE 274
 Db 233 INNSDLVAVNIETGEERLTFCHQGLSNVLDPKSAGVATPVLOEEDFSGVWMPKAE 292
 QY 275 TTPSGGCKILRLILEENDESEVEIIVTSPMLETRRADSFYRPTGTANPKVFKKSEIM 333
 Db 293 WEGSEGLKTLRLILEEVEDESEVEIIVHPSPALERTDGYRPRGSKPKIALKLAEPQ 352
 QY 334 IDAEGRIIDVDELQIPELLEFEGVEYARAGWTPDEKYAMSILDRSOTRLQIVLISP 393
 Db 353 TPOCKIVSTOEKELVQPFSSLFPKVEYIARAGWTRDGKVAWAMFLDRPOQWLVLPLP 412
 QY 394 ELFIPEDDVMQRILIESVPSAPLILEETDQIWINIHDFHFRPSH-BEELIEFTF 452
 Db 413 ALFTPESTNEORLASARAVPRVQYVVEEVTNAINVHDLTFEPQSEGDELCPKR 472
 QY 453 ASECKTGFPHLYKITSLLESKYKRSSGGLPAPSDKCPKEIEIATSGEMEWYLRHGSN 512
 Db 473 ANBCKTGFCHLYKVTAVLKSQGDWSEPPSPGDEDEKCKIEKIEIATSGEMEWYLRHGSN 532
 QY 513 IOYDEVRLRYFEGTKDSPLHLHYVSVNNGEYTRLDRTGYSHSCICSOHCDFIISKY 572
 Db 533 IWNNEETKLYFEGTKDPTLEHLHYVSVNNGEYTRLDRTGYSHSCICSOHCDFIISKY 592
 QY 573 SNOKNHCYSLKLSPPEDDPTCKTEKFNATLIDSGPLPDYTPRPFESFTGTLYG 632
 Db 593 SSYSTPPCYHVYKLSGPDPLHKKOPFNAMSEASCPDPYPRPEIFPHTRSDVRLVG 652
 QY 633 MLYKPHDLQPKKPYTLFETYGPOVOLVNNRFGVYRNLTLASLGVVWVINDRGSC 692
 Db 653 MLYKPHALQPKKHPYTLFETYGPOVOLVNNRFGVYRNLTLASLGVVWVINDRGSC 712
 QY 693 HNGKAFEGAFKTKMGQIEIDDOVEGLQYLAISKRDPLDRLVGIHGSYGYSLMALMOR 752
 Db 713 ORGLRFEGLAKNMGVEIEDQVEGLQFAEKYGFIDLSRVAIHGWSYGGFLSLMGLINK 772
 QY 753 SDIFRAVAGAPVTLWIFDGTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 812
 Db 773 POVFVAIAGAPVTVMAVDGTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 832

RESULT 16
 AAE24168
 ID AAE24168 standard; Protein: 969 AA.
 AC AAE24168;
 DT 23-SEP-2002 (first entry)
 DE Human dipeptidyl peptidase 9 (DPP9) protein.

Human: dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis; autoimmunity; human immunodeficiency virus; HIV infection; cytostatic; graft rejection; antidiabetic; antiinflammatory; immunosuppressive; antiviral; enzyme.

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XX OS Homo sapiens.
XX Key Location/Qualifiers
XX FT Misc-difference 374
XX FT /note= "Encoded by GAA"
XX PN WO200234900-A1.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001: 2001WO-AU01388.
XX PR 27-OCT-2000: 2000AU-0001078.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Abbott CA, Gorrell MD;
XX DR WPI: 2002-454646/48.
XX DR N-PSDB: AAD38954.
XX
XX PT New dipeptidyl peptidase (DPP) peptides, useful for screening
XX PT inhibitors of DPP catalytic activity, which may be employed to treat
XX PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX PT rejection and HIV infection.
XX PS Claim 1: Fig 4: 91pp; English.
XX CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
XX CC polynucleotides encoding such proteins. The DPP peptides are useful for
XX CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
XX CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX CC rejection and HIV (human immuno deficiency virus) infection. The present
XX CC sequence is human DPP9 protein.
XX SQ Sequence 969 AA:
XX
XX Query Match 60.9%; Score 2863; DB 23; Length 969;
XX Best Local Similarity 61.4%; Pred. No. 1.3e-266;
XX Matches 516; Conservative 134; Mismatches 188; Indels 2; Gaps 2;
XX
OY 35 FVYERSWSQKLKLDTRKRYHGMKAKAPHDFMFKRNDPDPHSDRIYLLAMSGENRE 94
OY 130 FQYQKSHSMGSLRSIIHSGSRKYSGLIVNKAAPHDFQVQKTDESGRHSRLYLGMPIGSR 189
OY 95 NTLFGEIPIKTIKRAVIMSMKRLDLPQATIDYGMYSREELLRRKRIQVGIASVD 134
OY 190 NSLTYSEIPKVKKEALLSLMKOMLDHFOATPHHGVYSREELLRRKRLGVGITSVD 249
OY 155 YHOGSGTFLFOAGSGIYHVKDGGPOGFTQOPLRNLYETSCPNIRMDPKLCPADPMIAF 214
OY 250 FHSSEGLFLFOAGNSLFLHCRDGGKNGFPMSPKRLKTKQCSGRPRDKCPADPAFFSF 309
OY 215 IHSNDIWSNIYVREERRLTYHNELANMEDARSAGVATFVLQEEBDRYSGYWCCKPAE 274
OY 310 NNSMDLWANIETGEERRLTFCHQGLSNVLDPKSAGVAFVIOEEDRFTGYWCCKPTAS 369
OY 275 TTPSGG-KILRIIYENDESEVHIIHTSPMLFTRRYPKGTGANPKVFFKSEIM 333
OY 370 WEGSQGLKRLRIIYEYDESEVYIVHPSPALERKIDSTRYPTGSKNKIKALIAEFO 429
OY 334 IDAEGRIIVIDKELIQPELLEGEVEYIARAGWTEGKYAMSILLDRSQTRLQIYLISP 393
OY 430 TDSQGLIVSIOEKELVQPSLSLFPKVEYIARAGWTGDKYAMMFLDRPQOMIQLVLLPP 489
OY 394 ELFIPEEDVMEQRLIESYVDSVPLIYEETDWINIHDFHVPPOSH-EEBIEFTF 452
OY 490 ALFIPESTNEEOGLASARAVPRNVQPYVVEYTNWIMVHDFIYFPPOSSEGDELCFLR 549
OY 453 ASBCKGFRHLVYKITSLESKYKRSRSGGLPAPSDKCPKKEIATISGWEVLGRHGSN 512
OY 550 ANECKTGFCFLKIVTAVLKSQGYDSEPPSPGDEKRCPIKEIATISGWEVLARHGSK 609

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OY 513 IQYDEVRLVYFEGTKDPSLEHHLVYVSNPEVTRLTDGYSHSCCIHQHCFPISKY 572
OY 610 IWNNEETKLIVFGCTKDTPLEHHLVYVSEAGEIYRLTTPGSHSCSNQNDMEVSHY 669
OY 573 SNQNPCHVSLKLSPPEDDPTCKTEFNATILDSAGLPDITPPIPSFESTGTLYG 632
OY 670 SSVSTPPCVHVVYKLSGPDDDPLKQRPFWASMEASCPEDVPYPIFFHFRSDRLVG 729
OY 633 MLKKPHDLPQCKKYPVTLFYGGPOVOLVNNRKKGVKRYFLNLTASLGAVVVIDNRGSC 692
OY 730 MTKPHALDPGKKNPTVLFYGGPOVOLVNNRKFGLIKRLNLTASLGAVVVIDNRGSC 789
OY 693 HRGLKFECAFVKYKMGQIEIDQVEGLQYLASRYDFIDLDRVGIHGSYGYLSLALMOR 752
OY 790 QRLRFEGALKNMQGVLEIDQVEGLQYFAEKYGFIDLSRVAIHGSYGYLSLALMOR 849
OY 753 SDIFRVAIAGAPVTLMIFFDGTTERYMGHPDQNEGGYLGVSAMQAEKFPSPENRLL 812
OY 850 PQYKVAIAGAPVTLVMVAVDTGYTERYMDVPENNQHGVEGSAVLAHVEKLPNEPRLL 909
OY 813 HGFLENVHFAHRSILSLFVLRAGKPYDLOIYPOERHSIRVPESGHEYLHLHYQENL 872
OY 910 HGFLENVHFAHRSILSLFVLRAGKPYDLOIYPOERHSIRCPESGHEYLHLHYQENL 969
XX
XX RESULT 17
XX ID AAE24171 standard; Protein: 830 AA.
XX AC AAE24171;
XX XX 23-SEP-2002 (first entry)
XX DT
XX DE Human dipeptidyl peptidase 4 (DPP4)-like 2 protein.
XX
XX KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
XX KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
XX KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
XX KW antiviral; enzyme; DPP-4 like 2 protein.
XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 235
XX FT /note= "Encoded by GAG"
XX
XX PN WO200234900-A1.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001: 2001WO-AU01388.
XX PR 27-OCT-2000: 2000AU-0001078.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Abbott CA, Gorrell MD;
XX DR WPI: 2002-454646/48.
XX DR N-PSDB: AAD38954.
XX
XX PT New dipeptidyl peptidase (DPP) peptides, useful for screening
XX PT inhibitors of DPP catalytic activity, which may be employed to treat
XX PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX PT rejection and HIV infection.
XX PS Disclosure; Page 82-86; 91pp; English.
XX CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
XX CC polynucleotides encoding such proteins. The DPP peptides are useful for
XX CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
XX CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft.

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DB 390 ALFPAVESEARQAAARAVPKNOPEVIEEVTNWMVNHDIHPPEQAOGODFCFLR 449
453 ASECRTGFRHLKYKTSILKESKYRRSSGGLPAPSDFCPIKEELTAISGEMEVLGRHGSN 512
450 ANECKTGCHLYKTYVLEKTKYDWMTEPLSTEGEFCPIKEEVALTSGEMEVLGRHGSK 509
513 IOVDEVRLVYFEGTKDSPLEHHLVYVSYVNGEVTRLTDGYSHSCCISOCHDFITISKY 572
510 IWNVEQKRLVYFQGTQDTPLEHHLVYVSYEAGELVRLTTGFSHSCSMQSFMEVSHY 569
573 SNOKNPHCVSLYKLSPEDDPTCKTEFWATILDSAGPLDPTPELTFSESTGFTLYG 632
570 SSVSTPPCVHYHKLSGDDPDLHQPFRFMASSMEANCPDPPYVPELTFHFTRADVQLYG 629
633 MLYRPHDLQPGKKPYTLFTFYGPQVOLLVNNRFGVKYFRNLTLASIGYVVYVDNRGSC 692
630 MLYRPHDLQPGKKPYTLFTFYGPQVOLLVNNRFGVKYFRNLTLASIGYVVYVDNRGSC 689
693 HRGLKEGAEFYKMGQIEIDDOVEGLQYLASRYDFIDLDRVGIHGSYGYLSMALMQR 752
690 QRGHFEGLALKNGQYIEIDQVEGLQYVAEKYFIDLSRAVHIGWSYGGFLSLMGLIHK 749
753 SDIRVALIAGAPVTLMTFYDTGTERYMGHPDQDQGYLGSVAMQAEKPFSEPNRLILL 812
750 PÖVEKVALIAGAPVTVMAYDGYTERYMDVPENNQGYEAGSVALHVEKLPNEPNRLILL 809
813 HGFIDENVHFAHTSILSEFLVRACKPYDLOIYPOERHSIRPESGEHEHLHLHYLOENT 872
810 HGFIDENVHFAHTSILSEFLVRACKPYDLOIYPOERHSIRPESGEHEHLHLHYLOENT 869

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RESULT 19

ABG61607
ID ABG61607 standard; Protein; 879 AA.

AC ABG61607;

DT 12-AUG-2002 (first entry)

XX Human DPRP-2 splice variant #6.

XX Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPY; Infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinestia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.

XX Homo sapiens.

OS MO200231134-A2.

PN 18-APR-2002

PD 12-OCT-2001; 2001WQ-US31874.

PF 12-OCT-2000; 2000US-240117P.

PR (FERR) FERRING BV.

PA Qi S, Akinsanya KO, Riviere PJ, Junien J;

XX WPI: 2002-444178/47.

XX DR N-PSDB; ABR83338.

PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 viral infections, cancers, allergies, neurological disorders, or pain

PS Disclosure; Page 91-93; 113pp; English.

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XX The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPY)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bilitia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinestias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ Sequence 879 AA;
Query Match 60.0%; Score 2820.5; DB 23; Length 879;
Best Local Similarity 60.7%; Pred. No. 1,4e-262;
Matches 510; Conservative 132; Mismatches 183; Indels 15; Gaps 3;
35 FVYERYSQSLKLLADTRKHGMAMKAPDPEVFNKNDPDGSHDRITYLANSGENRE 94
53 FÖYKHSMWGLRSIIHGRKYSGLIVNKAAPDFOVOKTGESGSHRLYGLMPGYSR 112
95 NTLFYSEIPTINRAAVYLMISMKPLDLFOATLDYGMYSREELLRRKRIGTVGASD 154
113 NSLYSELIPKVKREKALLLSMKOMLDFQATPIHGYVSRREELRRKRIGTVGASD 172
155 YHGGSGFLFQAGSGIYHVKDGPQGFQOPLRPNLVETSCPNTRMDPKLCPADPMIAF 214
173 FHSSEGLFQASNSLFRHCRDQKNGFVSPMKPLEIKTQSGRMDPKLCPADPAFFSF 232
215 IHSNDIMSNVTREERLTYVHNELANMEDASAGVATVLOEEDRDSGYWMCRAE 274
233 INNSDLWANLETGEERLTYFCHQGLSNVLDPPSAGVATVLOEEDRDSGYWMCRAE 292
275 TTPSGG-KILRIIYEENDESEVEIHTVSPMLERRRDSFPYPTGTPANPKVTFKMSIM 333
293 WESSEGLKTLRIILYEVDESEVEIHTVSPMLERRRDSFPYPTGTPANPKVTFKMSIM 352
334 IDAEGRIIDVIDKELIOPFETLFEVGEVYIARAGWTPBGKAWMSILLDRSOTRIQVILSP 393
353 TDSOGKIYSTEKELVOPFSSLPFKVEYIARAGWTPBGKAWMSILLDRSOTRIQVILSP 412
394 ELFPVDDWNERRLLESVDSTVPLIYEETDININIDIPHPPOSH-EEIEEIF 452
413 ALFIPSTENEBÖRLASARAVERNÖPYVVEEVTNWMVNHDIHPPEQAOGODFCFLR 472
453 ASECRTGFRHLKYKTSILKESKYRRSSGGLPAPSDFCPIKEELTAISGEMEVLGRHGSN 512
473 ANECKTGCHLYKTYVLEKTKYDWMTEPLSTEGEFCPIKEEVALTSGEMEVLGRHGSK 531
513 IOVDEVRLVYFEGTKDSPLEHHLVYVSYVNGEVTRLTDGYSHSCCISOCHDFITISKY 572
532 -----KGTQDTPLEHHLVYVSYEAGELVRLTTGFSHSCSMQSFMEVSHY 579
573 SNOKNPHCVSLYKLSPEDDPTCKTEFWATILDSAGPLDPTPELTFSESTGFTLYG 632
580 SSVSTPPCVHYHKLSGDDPDLHQPFRFMASSMEANCPDPPYVPELTFHFTRADVQLYG 639
633 MLYRPHDLQPGKKPYTLFTFYGPQVOLLVNNRFGVKYFRNLTLASIGYVVYVDNRGSC 692
640 MLYRPHDLQPGKKPYTLFTFYGPQVOLLVNNRFGVKYFRNLTLASIGYVVYVDNRGSC 699
693 HRGLKEGAEFYKMGQIEIDDOVEGLQYLASRYDFIDLDRVGIHGSYGYLSMALMQR 752
700 QRGHFEGLALKNGQYIEIDQVEGLQYVAEKYFIDLSRAVHIGWSYGGFLSLMGLIHK 759
753 SDIRVALIAGAPVTLMTFYDTGTERYMGHPDQDQGYLGSVAMQAEKPFSEPNRLILL 812
760 PÖVEKVALIAGAPVTVMAYDGYTERYMDVPENNQGYEAGSVALHVEKLPNEPNRLILL 819

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